

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2006, 21:41:48 ; Search time 53.6679 Seconds
(without alignments)
826.886 Million cell updates/sec

Title: US-10-815-562-2_COPY_31_131
Perfect score: 535
Sequence: 1 QVLSYKEAVLRADIGNQRS.....VTLNQARGSFDISCDKNR 101

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-----------|-------------|
| 1 | 535 | 100.0 | 140 | ADJ82974 | Human Pep |
| 2 | 535 | 100.0 | 152 | AAG03781 | Human sec |
| 3 | 535 | 100.0 | 169 | ADK70797 | Human CAP |
| 4 | 535 | 100.0 | 170 | AAR92924 | Prepro-PA |
| 5 | 535 | 100.0 | 170 | AAB07901 | A human c |
| 6 | 535 | 100.0 | 170 | ABB07707 | Human pep |
| 7 | 535 | 100.0 | 170 | Aau90996 | Transplan |
| 8 | 535 | 100.0 | 170 | ADP18219 | Protein s |
| 9 | 535 | 100.0 | 170 | ADP65263 | Human cat |
| 10 | 535 | 100.0 | 170 | AD129582 | Human CAP |
| 11 | 535 | 100.0 | 170 | ADJ82973 | Human Pep |
| 12 | 535 | 100.0 | 170 | ADN41827 | Human L |
| 13 | 535 | 100.0 | 170 | ADR47315 | Human cat |
| 14 | 535 | 100.0 | 170 | ABM80449 | Tumour-as |
| 15 | 535 | 100.0 | 170 | ADW43827 | Mouse che |
| 16 | 535 | 100.0 | 170 | ADX08374 | Cathelic |
| 17 | 535 | 100.0 | 170 | ADZ80363 | Human cat |
| 18 | 475 | 88.8 | 177 | AEA031061 | Novel hum |
| 19 | 408 | 76.3 | 170 | AEA00315 | Human cat |
| 20 | 367 | 68.6 | 170 | Aau90997 | Transplan |
| 21 | 367 | 68.6 | 170 | ADX08375 | Myeloid c |
| 22 | 364 | 68.0 | 156 | Aau90999 | Transplan |
| 23 | 364 | 68.0 | 156 | ADX08377 | Myeloid c |
| 24 | 361 | 67.5 | 176 | ADZ80368 | Goat cath |

| | | | | | | |
|----|-------|------|-----|---|----------|-----------|
| 25 | 354 | 66.2 | 155 | 5 | ABB07704 | Bovine pe |
| 26 | 354 | 66.2 | 155 | 5 | Aau90993 | Transplan |
| 27 | 354 | 66.2 | 155 | 9 | ADX08371 | Bactenecl |
| 28 | 352.5 | 65.9 | 159 | 5 | Aau90998 | Transplan |
| 29 | 352.5 | 65.9 | 159 | 5 | ADX08376 | BMAP-28 m |
| 30 | 350 | 65.4 | 172 | 9 | ADZ80367 | PR-39 pol |
| 31 | 347 | 64.9 | 147 | 2 | Aau18158 | Antimicro |
| 32 | 347 | 64.9 | 147 | 8 | ADL18364 | Pig prote |
| 33 | 347 | 64.9 | 149 | 2 | AAW25081 | Antimicro |
| 34 | 347 | 64.9 | 149 | 2 | AAW18157 | Antimicro |
| 35 | 347 | 64.9 | 149 | 2 | AAW18156 | Antimicro |
| 36 | 347 | 64.9 | 149 | 2 | Aau90987 | Antimicro |
| 37 | 347 | 64.9 | 149 | 2 | Aau18159 | Antimicro |
| 38 | 347 | 64.9 | 149 | 8 | ADL18362 | Pig prote |
| 39 | 347 | 64.9 | 149 | 8 | ADL18366 | Pig prote |
| 40 | 347 | 64.9 | 149 | 8 | ADL18368 | Pig prote |
| 41 | 343 | 64.1 | 142 | 8 | ADK70796 | Rabbit CA |
| 42 | 343 | 64.1 | 171 | 5 | ABB07703 | Rabbit pe |
| 43 | 340.5 | 63.6 | 160 | 5 | Aau91000 | Transplan |
| 44 | 340.5 | 63.6 | 160 | 9 | ADX08378 | SMAP 29 a |
| 45 | 340 | 63.6 | 176 | 5 | ABB07705 | Bovine pe |

ALIGNMENTS

RESULT 1
ADJ82974
ID ADJ82974 standard; protein; 140 AA.
XX
AC ADJ82974;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human Pep714-related peptide precursor SEQ ID NO: 2.
XX
KW pep714-related peptide; precursor; human; secreted peptide; Pep714;
KW oral mucositis; oral lesion; cystic fibrosis; respiratory infection;
KW pneumonia.
XX
OS Homo sapiens.
XX
PN WO2004005338-A1.
XX
PD 15-JAN-2004.
XX
PF 30-JUN-2003; 2003WO-EP006930.
XX
PR 08-JUL-2002; 2002US-0394486P.
PR 07-JAN-2003; 2003US-0438602P.
(GENE-) GENEPROT INC.
PI Bougueleret L, Jeandenans C, Niknejad A;
XX
WPI; 2004-099371/10.
DR
PT Novel Pep714-related polypeptide having biological activity, useful for
PT treatment and prevention of microbial or viral infection, cystic fibrosis
PT and chronic respiratory infections.
XX
PS Disclosure; Page 92-93; 99pp; English.
XX
CC The present invention relates to a Pep714-related peptide. This is useful
CC for inhibiting microbial propagation, preferably viral propagation, and
CC in the treatment of chemotherapy and radiotherapy induced oral mucositis,
CC oral lesion, ventilator associated pneumonia, chronic respiratory
CC infections and cystic fibrosis. The present sequence is a Pep714-related
XX peptide precursor protein shown in the exemplification of the invention.
SQ Sequence 140 AA;
Query Match 100.0%; Score 535; DB 8; Length 140;

```
Best Local Similarity 100.0%; Pred. No. 9.6e-57;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVLSYKEAVLRAIDGINORSSDANLYRLDLLDPRPTMDGDDPTPKPVSVFTVKETVCPRTT 60
DB 1 QVLSYKEAVLRAIDGINORSSDANLYRLDLLDPRPTMDGDDPTPKPVSVFTVKETVCPRTT 60
QY 61 QQSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDKNR 101
DB 61 QQSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDKNR 101

RESULT 2
AAG03781
ID AAG03781 standard; protein; 152 AA.
XX
AC AAG03781;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein, SEQ ID NO: 7862.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-00200610.
XX
PR 26-FEB-1999; 99US-0122487P.
XX
PA (GEST ) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX
DR WPI; 2000-500381/45.
XX
DR N-PSDB; AAC03787.
XX
New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
PS Claim 13; SEQ ID NO 7862; 71pp + Sequence Listing; English.
XX
The present sequence is a polypeptide encoded by one of a large number of
CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
CC tissues. EST sequences usually correspond mainly to the 3' untranslated
CC region (UTR) of the mRNA because they are often obtained from oligo-dT
CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
CC sequences derived from the 5' ends of mRNAs and even in those cases where
CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
CC are also used in diagnostic, forensic, gene therapy and chromosome
CC mapping procedures. They are used to obtain upstream regulatory sequences
CC and to design expression and secretion vectors
XX
SQ Sequence 152 AA;

Query Match 100.0%; Score 535; DB 3; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.1e-56;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVLSYKEAVLRAIDGINORSSDANLYRLDLLDPRPTMDGDDPTPKPVSVFTVKETVCPRTT 60
DB 34 QVLSYKEAVLRAIDGINORSSDANLYRLDLLDPRPTMDGDDPTPKPVSVFTVKETVCPRTT 93
QY 61 QQSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDKNR 101

Best Local Similarity 100.0%; Pred. No. 9.6e-57;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVLSYKEAVLRAIDGINORSSDANLYRLDLLDPRPTMDGDDPTPKPVSVFTVKETVCPRTT 60
DB 1 QVLSYKEAVLRAIDGINORSSDANLYRLDLLDPRPTMDGDDPTPKPVSVFTVKETVCPRTT 60
QY 61 QQSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDKNR 101
DB 61 QQSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDKNR 101

RESULT 3
ADK70797
ID ADK70797 standard; protein; 169 AA.
XX
AC ADK70797;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human CAPI8 full-length protein.
XX
KW alpha-helix; thionine; antibacterial; antifungal; plant;
KW fungi resistance; rice blast fungus; Ceratocystis fimbriata; bacteria;
KW Pseudomonas; antimicrobial; rabbit; CAPI8.
XX
OS Homo sapiens.
XX
PN JP2003204794-A.
XX
PD 22-JUL-2003.
XX
PF 15-JAN-2002; 2002JP-00006607.
XX
PR 15-JAN-2002; 2002JP-00006607.
XX
PA (TOYW ) TOYOTA CHUO KENKYUSHO KK.
XX
DR WPI; 2004-102620/11.
XX
Antimicrobial polypeptide composition for a plant pathogen, comprises one
PT or more types of thionine and/or a polypeptide having an alpha helix
PT structure, as an active ingredient.
XX
PS Disclosure; SEQ ID NO 38; 27pp; Japanese.
XX
The invention relates to a novel polypeptide composition for preventing
CC disease in an organism which comprises one or more types of polypeptide
CC which have an alpha-helix structure and/or thionine component. The
CC composition of the invention demonstrates antibacterial and antifungal
CC activities and may be useful for preventing a disease in an organism, for
CC generating cultivated plants and in providing resistance to plant tissue
CC against fungi such as Pyricularia oryzae (rice blast fungus),
CC Ceratocystis fimbriata and bacteria such as Pseudomonas etc. The
CC composition has high antimicrobial activity at low concentration. The
CC current sequence is that of the rabbit CAPI8 full-length protein of the
CC invention.
XX
SQ Sequence 169 AA;

Query Match 100.0%; Score 535; DB 8; Length 169;
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVLSYKEAVLRAIDGINORSSDANLYRLDLLDPRPTMDGDDPTPKPVSVFTVKETVCPRTT 60
DB 31 QVLSYKEAVLRAIDGINORSSDANLYRLDLLDPRPTMDGDDPTPKPVSVFTVKETVCPRTT 90
QY 61 QQSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDKNR 101
DB 91 QQSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDKNR 131

RESULT 4
AAR92924
ID AAR92924 standard; protein; 170 AA.
XX
AC AAR92924;
XX
DT 06-JUN-1996 (first entry)
XX
```

DE Prepro-FALL-99.
 XX FALL-39; cathelin; antibiotic; antimicrobial; antibacterial.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..131
 FT Protein /label= Prepro-peptide
 FT 132..170
 FT /label= FALL-39
 FN WO9608508-A1
 XX
 PD 21-MAR-1996.
 XX
 PF 12-SEP-1995; 95WO-SE001030.
 XX
 PR 13-SEP-1994; 94SE-00003055.
 XX
 PA (BOWA/) BOWAN H G.
 PI Agerberth B, Gudmundsson GH, Gunne H;
 DR WPI; 1996-179899/18.
 DR N-PSDB; AAT18233.
 XX
 XX Novel peptide antibiotic, FALL-39 - overcomes classical antibiotic resistance and is non-cytotoxic.
 XX Example 2; Fig 1; 26pp; English.
 XX
 CC Novel cathelin-like prepro-FALL-39 (AAR92924) is the precursor of the antimicrobial, antibacterial agent FALL-39 (see AAR92923). It is the product of a cDNA clone (AAT18233) isolated from a human bone marrow cDNA library. FALL-39 includes a helical region (see AAR92922) that is required for biological activity. FALL-39 is useful therapeutically for inhibiting microbial growth in mammals, including humans, and is non-cytotoxic
 XX
 SQ Sequence 170 AA;
 Query Match 100.0%; Score 535; DB 2; Length 170;
 Best Local Similarity 100.0%; Pred. No. 1.2e-56;
 Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QVLSYKEAVLRAIDGINQRSSDANLYRLDLDPRPTMDGDDPTPKPVSTVKTVCPRTT 60
 DB 31 QVLSYKEAVLRAIDGINQRSSDANLYRLDLDPRPTMDGDDPTPKPVSTVKTVCPRTT 90
 QY 61 QQSPEDCDFKXGGLVKRCMGTTVLNQARGSFDISCDKNKR 101
 DB 91 QQSPEDCDFKXGGLVKRCMGTTVLNQARGSFDISCDKNKR 131
 RESULT 5
 AAB07901
 ID AAB07901 standard; protein; 170 AA.
 XX
 AC AAB07901;
 XX
 DT 14-NOV-2000 (first entry)
 XX
 DE A human cationic protein designated CAP18.
 XX
 KW Human; cationic protein; lipopolysaccharide binding; anticoagulant;
 KW CAP18; reactive nitrogen inhibitory protein; RNIP; gram negative sepsis;
 KW coagulation-related disorder; disseminated intravascular coagulation.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Protein 134..170

/note= "reactive nitrogen inhibitory protein"

US6103888-A.
 15-AUG-2000.
 01-JUN-1999; 99US-00322911.
 17-JUL-1992; 92US-00916761.
 17-JUL-1992; 92US-00916765.
 15-JUL-1993; 93WO-US006731.
 27-SEP-1994; 94US-00313681.
 01-AUG-1996; 96US-00691280.
 (PANO-) PANORAMA RES INC.
 Larrick JW, Wright SC, Hirata M;
 WPI; 2000-531989/48.
 N-PSDB; AAR59574.
 Novel human cDNA encoding cationic proteins having lipopolysaccharide binding and anticoagulant activity, useful for treating and diagnosing gram negative sepsis and disseminated intravascular coagulation.
 Disclosure; Col 29-30; 46pp; English.
 The present sequence represents a human cationic protein, having lipopolysaccharide binding and anticoagulant activity. The polypeptide is designated CAP18. Amino acids 134-170 of CAP18 represent a reactive nitrogen inhibitory protein (RNIP). The CAP18 polynucleotide is useful for producing cationic proteins. The CAP18 polypeptide is useful for treating and diagnosing lipopolysaccharide-associated conditions such as gram negative sepsis, and/or coagulation-related disorders, such as disseminated intravascular coagulation
 Sequence 170 AA;
 Query Match 100.0%; Score 535; DB 3; Length 170;
 Best Local Similarity 100.0%; Pred. No. 1.2e-56;
 Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QVLSYKEAVLRAIDGINQRSSDANLYRLDLDPRPTMDGDDPTPKPVSTVKTVCPRTT 60
 DB 31 QVLSYKEAVLRAIDGINQRSSDANLYRLDLDPRPTMDGDDPTPKPVSTVKTVCPRTT 90
 QY 61 QQSPEDCDFKXGGLVKRCMGTTVLNQARGSFDISCDKNKR 101
 DB 91 QQSPEDCDFKXGGLVKRCMGTTVLNQARGSFDISCDKNKR 131
 RESULT 6
 ABB07707
 ID ABB07707 standard; peptide; 170 AA.
 XX
 AC ABB07707;
 XX
 DT 10-JUN-2002 (first entry)
 XX
 DE Human peptide antibiotic FALL-39 precursor sequence.
 XX
 KW Vaccine; cathelicidin; antimicrobial; immunostimulant; immune response;
 KW antigen presenting cell; adjuvant; human; antibiotic; FALL-39.
 XX
 OS Homo sapiens.
 XX
 FN WO200213857-A2.
 PD 21-FEB-2002.
 XX
 PF 17-AUG-2001; 2001WO-EP009529.
 XX
 PR 17-AUG-2000; 2000AT-00001416.

XX (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
XX
XX Fritz J, Mattner F, Zauner W, Buschle M, Egyed A;
PI
XX WPI; 2002-269154/31.
DR
XX
XX Vaccine for active immunization or for preparing an adjuvant for
PT enhancing an immune response to at least one antigen, comprises at least
PT one antigen and at least one cathelicidin derived antimicrobial peptide.
XX
XX Disclosure; Fig 1; 65pp; English.
XX
XX The invention relates to a vaccine comprising at least one antigen and at
CC least one cathelicidin derived antimicrobial peptide or its derivative.
CC The vaccine is useful for active immunization, especially of humans or
CC animals without protection against the specific antigen. The cathelicidin
CC derived antimicrobial peptide is useful in the preparation of an adjuvant
CC for enhancing the immune response to at least one antigen, where the
CC adjuvant enhances the uptake of at least one antigen in antigen
CC presenting cells (APC), and the adjuvant is added to the vaccine.
CC Sequences AB807701-07 represent cathelicidin proteins form various
CC species
XX
XX Sequence 170 AA;
SQ
Query Match 100.0%; Score 535; DB 5; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QVLSYKAVLRRAIDGINQRSSDANLYRLDLLDPRPTMDGDDTPKPVSVFTVKETVCPRTT 60
Db 31 QVLSYKAVLRRAIDGINQRSSDANLYRLDLLDPRPTMDGDDTPKPVSVFTVKETVCPRTT 90
Qy 61 QQSPEDCDFKKGVLKRCMGVTTLNQARGSFDISCDKNKR 101
Db 91 QQSPEDCDFKKGVLKRCMGVTTLNQARGSFDISCDKNKR 131
RESULT 7
ID AAU90996 standard; peptide; 170 AA.
AC AAU90996;
XX
XX 05-JUN-2002 (first entry)
DT
XX Transplant media associated antimicrobial peptide #32.
XX Transplant; antimicrobial peptide; pore forming agent;
XX cell surface receptor binding compound; kidney transplant; cardioplegia;
KW organ transplant; transplant rejection.
XX Homo sapiens.
OS
XX WO200209738-A1.
PN
XX 07-FEB-2002.
FD
XX 27-JUL-2001; 2001WO-US023785.
XX
XX 28-JUL-2000; 2000US-0221632P.
PR
XX 17-NOV-2000; 2000US-0249602P.
PR
XX 15-MAY-2001; 2001US-0290932P.
XX
XX (MURPHY) MURPHY C J.
PA
XX Murphy CJ, Reid TW, Mcanulty JP;
PI
XX WPI; 2002-268995/31.
XX
XX Media comprising antimicrobial polypeptides or pore forming agents and/or
PT cell surface receptor binding compounds useful for the storage and
PT

PT preservation of organs prior to transplant.
XX Disclosure; Page 27; 78pp; English.
XX
XX The invention describes new transplant compositions comprising
CC antimicrobial polypeptides or pore forming agents and/or cell surface
CC receptor binding compounds. The media is capable of extending the
CC preservation period past 72 hours and can provide organs with increased
CC functionality upon transplant. Animals receiving kidneys stored in the
CC media of the present invention for either three or four days had serum
CC creatinine levels of less than half of those observed in control animals
CC receiving kidneys stored in UW solution (defined in the specification)
CC alone. Lower serum creatinine levels are indicative of healthier kidneys
CC and a more preferable prognosis for the transplant patient. The media of
CC the invention are useful for decreasing the incidence and/or severity of
CC delayed graft function in patients receiving transplanted kidneys stored
CC and/or treated in the media. The media may also be used in procedures
CC such as cardioplegia. It is contemplated that transplant of healthier
CC organs leads to a decrease in chronic rejection. This sequence represents
CC an antimicrobial peptide studied in the development of the transplant
XX media
XX
XX Sequence 170 AA;
SQ
Query Match 100.0%; Score 535; DB 5; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QVLSYKAVLRRAIDGINQRSSDANLYRLDLLDPRPTMDGDDTPKPVSVFTVKETVCPRTT 60
Db 31 QVLSYKAVLRRAIDGINQRSSDANLYRLDLLDPRPTMDGDDTPKPVSVFTVKETVCPRTT 90
Qy 61 QQSPEDCDFKKGVLKRCMGVTTLNQARGSFDISCDKNKR 101
Db 91 QQSPEDCDFKKGVLKRCMGVTTLNQARGSFDISCDKNKR 131
RESULT 8
ID ADF18219 standard; protein; 170 AA.
AC ADF18219;
XX
XX 12-FEB-2004 (first entry)
DT
XX Protein sequence.
DE
XX Antimicrobial; LL-37; hCAP-18; antiarteriosclerotic; antiulcer;
KW vulnery; cytostatic.
XX Unidentified.
OS
XX Key Location/Qualifiers
FH Misc-difference 6 /note= "Encoded by AAT"
FT
XX EPI358888-A1.
PN
XX 05-NOV-2003.
XX
XX 27-FEB-2003; 2003EP-00004306.
PD
XX 28-FEB-2002; 2002EP-00004656.
PR
XX (BALS/) BALS R.
PA (KOCZ/) KOCZULLA A R.
XX (VDEG/) VON DEGENFELD G.
PA
XX Bals R, Koczulla AR, Von Degenfeld G;
PI
XX WPI; 2003-879818/82.
DR
XX N-PSDB; ADF18220.
XX

PT Use of a peptide LL-37 for the preparation of a composition for
 PT preventing or treating wounds or a disease caused reduced blood flow,
 PT e.g. atherosclerosis, coronary heart disease, stroke, arterial occlusive
 PT diseases or ulcer.

XX Disclosure; Page; 15pp; English.

XX The present invention is based on the finding that human antimicrobial
 CC peptide LL-37 ADP18218 is capable of inducing functionally important
 CC angiogenesis in cell culture and in vivo by activation of the receptor
 CC molecule FPRL1. LL-37 can be used in the preparation of a pharmaceutical
 CC composition for the prevention or treatment of a disease caused by, or
 CC resulting in, a reduced level of angiogenesis or arteriogenesis, or for
 CC the treatment of (infected) wounds or cancer. The disease may be
 CC associated with reduced blood flow, such as atherosclerosis, coronary
 CC heart disease, stroke, arterial occlusive disease or an ulcer.
 CC Suppression of angiogenesis through inhibition of LL-37 can be used to
 CC treat tumours, especially a carcinoma or sarcoma including cancer of the
 CC bile duct, brain, breast, colon, stomach, male and female reproductive
 CC organs, lung and airways, skin, gallbladder, liver, nasopharynx, nerve
 CC cells, kidney, prostate, and Kaposi's sarcoma (all claimed). The present
 CC protein sequence is not explained in the specification.

XX Sequence 170 AA;

Query Match 100.0%; Score 535; DB 7; Length 170;
 Best Local Similarity 100.0%; Pred. No. 1.2e-56;
 Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVLSYKEAVLRADGINQRSSDANLYRLDLLDPRPTMDGDDTPKPVSTTKETVCPRRT 60
 DB 31 QVLSYKEAVLRADGINQRSSDANLYRLDLLDPRPTMDGDDTPKPVSTTKETVCPRRT 90

QY 61 QQSPEDCDFKKGVLKRCMGTVTLNQARGSPDISCDKNKR 101
 DB 91 QQSPEDCDFKKGVLKRCMGTVTLNQARGSPDISCDKNKR 131

RESULT 9

ID ADP65263
 XX ADP65263 standard; protein; 170 AA.

AC ADP65263;

XX 12-AUG-2004 (first entry)

DE Human cathelicidin antimicrobial peptide. ✓

XX autoimmune disease; arthritis; gene expression analysis;
 KW rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;
 KW antiarthritic; osteopathic; antigout; antiinflammatory; dermatological;
 KW immunomodulatory; lupus; ankylosing spondylitis; fibrositis;
 KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
 KW immune; human.

XX Homo sapiens.

XX WO2003072827-A1.

XX 04-SEP-2003. ✓

XX 31-OCT-2002; 2002WO-US035433.

XX 31-OCT-2001; 2001US-0336220P.

XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

XX Hirsch R, Thorton SL;

XX WPI; 2003-712740/67.

XX GENBANK, NP_004336.

PT Diagnosing and analyzing autoimmune disease using gene expression

PT profiles and microarray technology, useful for diagnosing and treating
 PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
 PT gout.

XX Disclosure; Page; 56pp; English.

XX The invention relates to a novel method for diagnosing and analysing a
 CC autoimmune disease or arthritides. The method comprises obtaining a
 CC patient sample containing mRNA, analysing gene expression using the mRNA
 CC that results in a gene expression signature of the mRNA, and using that
 CC gene expression signature to diagnose or analyse the autoimmune disease
 CC or arthritides in the patient, where gene expression of at least 60% of
 CC the genes correlates with that of the gene signature. The invention
 CC further comprises: a treatment of rheumatoid arthritis; identification of
 CC genes for targeting in the treatment of rheumatoid arthritis in a mammal
 CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
 CC array or gene chip, specific for rheumatoid arthritis; diagnosis or
 CC analyses of autoimmune disease or rheumatoid arthritis; screening the
 CC efficacy of a candidate drug in vitro for the treatment of collagen-
 CC induced arthritis; and reducing the symptoms associated with collagen-
 CC induced arthritis. The compositions of the invention have the following
 CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,
 CC antigout, antiinflammatory, dermatological, and immunomodulatory. The
 CC methods and compositions of the present invention are useful for
 CC diagnosing and treating autoimmune disease or arthritides, such as
 CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
 CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
 CC immune disease caused by an infectious agent. This sequence represents a
 CC protein sequence relating to the genes used in the analysis and treatment
 CC of autoimmune diseases or arthritides. Note: This sequence is not shown
 CC in the specification. It has been supplied in an electronic format from
 CC WIPO.

XX Sequence 170 AA;

Query Match 100.0%; Score 535; DB 7; Length 170;

Best Local Similarity 100.0%; Pred. No. 1.2e-56;

Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVLSYKEAVLRADGINQRSSDANLYRLDLLDPRPTMDGDDTPKPVSTTKETVCPRRT 60

DB 31 QVLSYKEAVLRADGINQRSSDANLYRLDLLDPRPTMDGDDTPKPVSTTKETVCPRRT 90

QY 61 QQSPEDCDFKKGVLKRCMGTVTLNQARGSPDISCDKNKR 101

DB 91 QQSPEDCDFKKGVLKRCMGTVTLNQARGSPDISCDKNKR 131

RESULT 10

AD129582

ID AD129582 standard; protein; 170 AA.

XX AC AD129582;

XX 22-APR-2004 (first entry)

XX Human CAPI8, SEQ ID 4.

XX CAPI8; cationic antimicrobial protein of 18 kDa; bacterial pneumonia;
 KW chronic lung disease; acute lung disease; inflammatory lung disease;
 KW ARDS; bronchial asthma; human.

XX Homo sapiens.

XX WO2004009640-A1.

XX 29-JAN-2004.

XX 22-JUL-2003; 2003WO-JP009267.

XX 22-JUL-2002; 2002JP-00213040.

XX 14-MAR-2003; 2003JP-00070932.

PA (SEKG) SEIKAGAKU CORP.
PI Kirikae T, Toyooka K, Naiki Y, Tamura H, Ishizaka A, Hashimoto S;
XX WPI; 2004-143269/14.
XX
XX New antibody against an antibacterial peptide, particularly human CAP18,
PT applicable in reagents and kits for detection, diagnosis and monitoring
XX of bacterial pneumonia.
XX
PS Disclosure; SEQ ID NO 4; 52pp; Japanese.
XX
XX The present invention relates to a novel CAP18 (cationic antimicrobial
CC protein of 18 kDa) antibody that can bind with human CAP18 peptide
CC fragments AD129579-AD129581. The antibody is useful in reagents and kits
CC for the detection, diagnosis and monitoring bacterial pneumonia and other
CC CAP18-related diseases like chronic and acute lung diseases, inflammatory
CC lung diseases, ARDS and bronchial asthma. The present sequence is human
CC CAP18.
XX
XX Sequence 170 AA;
SQ
Query Match 100.0%; Score 535; DB 8; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLPRTMDGDDPTPKPVSVFTVKETVCPRTT 60
DB 31 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLPRTMDGDDPTPKPVSVFTVKETVCPRTT 90
QY 61 QQSPEDCDFKKGGLVKRCMGVTTLNQARGSPDISCDKDKNR 101
DB 91 QQSPEDCDFKKGGLVKRCMGVTTLNQARGSPDISCDKDKNR 131
RESULT 11
ADJ82973
ID ADJ82973 standard; protein; 170 AA.
XX
AC ADJ82973;
XX
XX 06-MAY-2004 (first entry)
XX
XX Human Pep714-related peptide precursor SEQ ID NO: 1.
XX
XX pep714-related peptide; precursor; human; secreted peptide; Pep714;
KW oral mucositis; oral lesion; cystic fibrosis; respiratory infection;
KW pneumonia.
XX
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..30
FT Protein 31..131 /label= signal_peptide
FT Cleavage-site 106..107 /label= propeptide
FT /note
FT /note= "dibasic peptidase cleavage site"
FT Cleavage-site 130..131 /note
FT /note
FT /note= "dibasic peptidase cleavage site"
FT Protein 132..170 /label= antibacterial_protein_FALL-39
FT Protein 134..170 /label= antibacterial_protein_LL-37
FT Cleavage-site 140..141 /note
FT /note= "dibasic peptidase cleavage site"
FT Cleavage-site 151..152 /note
FT /note= "dibasic peptidase cleavage site"
XX

PN WO2004005338-A1.
XX
XX 15-JAN-2004.
XX
PF 30-JUN-2003; 2003WO-EP006930.
XX
PR 08-JUL-2002; 2002US-0394486P.
PR 07-JAN-2003; 2003US-0438602P.
XX
PA (GENE-) GENEPROT INC.
XX
XX Bougueleret L, Jeandenans C, Niknejad A;
PI WPI; 2004-099371/10.
XX
XX Novel Pep714-related polypeptide having biological activity, useful for
PT treatment and prevention of microbial or viral infection, cystic fibrosis
PT and chronic respiratory infections.
XX
PS Disclosure; Page 91-92; 99pp; English.
XX
XX The present invention relates to a Pep714-related peptide. This is useful
CC for inhibiting microbial propagation, preferably viral propagation, and
CC in the treatment of chemotherapy and radiotherapy induced oral mucositis,
CC oral lesion, ventilator associated pneumonia, chronic respiratory
CC infections and cystic fibrosis. The present sequence is a Pep714-related
CC peptide precursor protein shown in the exemplification of the invention.
XX
XX Sequence 170 AA;
SQ
Query Match 100.0%; Score 535; DB 8; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLPRTMDGDDPTPKPVSVFTVKETVCPRTT 60
DB 31 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLPRTMDGDDPTPKPVSVFTVKETVCPRTT 90
QY 61 QQSPEDCDFKKGGLVKRCMGVTTLNQARGSPDISCDKDKNR 101
DB 91 QQSPEDCDFKKGGLVKRCMGVTTLNQARGSPDISCDKDKNR 131
RESULT 12
ADN41827
ID ADN41827 standard; protein; 170 AA.
XX
AC ADN41827;
XX
XX 15-JUL-2004 (first entry)
XX
XX Human LL-37 protein SEQ ID NO:2.
XX
XX infection; cathelicidin type peptide; LL-37; antimicrobial;
KW antiinflammatory; immunostimulant; bacterial infection; neutropenia;
KW toothpaste; mouthwash; gingivitis; oral infection; periodontitis; human.
XX
XX Homo sapiens.
XX
XX WO2004034061-A2.
XX
XX 22-APR-2004.
XX
PF 10-OCT-2003; 2003WO-EP011240.
XX
PR 10-OCT-2002; 2002GB-00023655.
XX
XX (MABT-) MABTECH AB.
XX
XX Bonan H, Andersson M, Puetsep K, Carlsson G;
PI WPI; 2004-364936/34.
XX
XX N-PSDB; ADN41826.
DR

XX Determination of susceptibility of subject to infection comprising
PT detecting cathelicidin type peptide present in sample, optionally
PT comparing level of peptide in sample to control sample.
XX
XX Disclosure; SEQ ID NO 2; 40pp; English.
XX
XX The present invention describes a method for determining the
CC susceptibility of a subject to infection. The method comprises: (i)
CC providing a sample from a subject; (ii) detecting any cathelicidin type
CC peptide (LL-37) present in the sample; (iii) optionally comparing the
CC level of LL-37 in the sample to a control sample; (iv) determining the
CC susceptibility of the subject to infection (where no LL-37 or a low level
CC of LL-37 indicates that subject is susceptible to infection); and (v)
CC optionally administering an antimicrobial agent to reduce infection. Also
CC described is a product containing LL-37 and a cytostatic drug,
CC corticosteroid or growth factor (preferably recombinant granulocyte
CC colony stimulating factor (G-CSF) or GM-CSF). The product has
CC antimicrobial, antiinflammatory and immunostimulant activities. The
CC method can be used for determining the susceptibility of a subject to
CC infection such as bacterial infection (e.g. Actinobacillus
CC actinomycetemcomitans infection) and neutropenia, and for diagnosing
CC neutropenia (e.g. Kostmann morbus). The method is also useful in the
CC manufacture of a medicament in the form of toothpaste or mouthwash for
CC the preventative treatment of infection e.g. gingivitis, oral infection
CC (such as periodontitis), and for the treatment of neutropenia. The method
CC controls the normal flora in neutropenia and so combat infections. The
CC present sequence represents the proform of human LL-37, which is used in
CC the exemplification of the present invention.
XX
XX Sequence 170 AA;
SQ
Query Match 100.0%; Score 535; DB 8; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLPRTMDGDPDTPKPVSTVKETVCPRTT 60
Db 31 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLPRTMDGDPDTPKPVSTVKETVCPRTT 90
QY 61 QQSPEDCDFKXGGLVKRCMGVTTLNQARGSPDISCDKNKR 101
Db 91 QQSPEDCDFKXGGLVKRCMGVTTLNQARGSPDISCDKNKR 131
RESULT 13
ADR47315
ID ADR47315 standard; protein; 170 AA.
XX
XX ADR47315;
XX
XX 18-NOV-2004 (first entry)
XX
XX Human cationic antimicrobial protein-18.
XX
XX cystic pulmonary fibrosis; cationic antimicrobial protein; CAP18;
XX pulmonary disease.
XX
XX Homo sapiens.
OS
XX JP2004245842-A.
FN
XX 02-SEP-2004.
PD
XX 13-FEB-2004; 2004JP-00036471.
PF
XX 14-FEB-2003; 2003US-0447310P.
PR
XX (SEKG) SEIKAGAKU KOGYO CO LTD.
PA
XX WPI; 2004-629858/61.
DR
XX Evaluating cystic pulmonary fibrosis, by measuring cationic antimicrobial

PT protein of 18 kDa (CAP18) quantity in biological sample, and evaluating
PT fibrosis by comparing measured quantity and quantity of CAP18 in control
PT sample.
XX
XX Disclosure; SEQ ID NO 4; 14pp; Japanese.
XX
XX The invention relates to a novel method for evaluating cystic pulmonary
CC fibrosis. The method comprises: measuring the quantity of cationic
CC antimicrobial protein of 18 kDa (CAP18) in the biological sample
CC collected from the individual; comparing the quantity of CAP18 measured
CC in the previous step and the quantity of CAP18 in a control sample; and
CC evaluating cystic pulmonary fibrosis by associating comparison of
CC obtained results. The invention further comprises: a kit for carrying out
CC the evaluating method, comprising a solid-phase component and an antibody
CC coupled with an antigenic peptide having a sequence of ADR47312, or a
CC solid-phase component comprising an immobilised antibody (first antibody)
CC which is coupled with the antigenic peptide, and the antibody (second
CC antibody) coupled with the antigenic peptide. The method or kit are
CC useful for evaluating cystic pulmonary fibrosis in an individual, where
CC the evaluation includes diagnosis for the presence or absence of a risk
CC of cystic pulmonary fibrosis, evaluation of serious or acute conditions,
CC or the evaluation of the advanced grade of the disease. The method
CC enables simple, cost-effective, rapid, highly sensitive and highly
CC accurate evaluation of the acute or serious conditions, or the
CC advancement of the pulmonary diseases. This sequence represents the human
CC CAP18 protein of the invention.
XX
XX Sequence 170 AA;
SQ
Query Match 100.0%; Score 535; DB 8; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLPRTMDGDPDTPKPVSTVKETVCPRTT 60
Db 31 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLPRTMDGDPDTPKPVSTVKETVCPRTT 90
QY 61 QQSPEDCDFKXGGLVKRCMGVTTLNQARGSPDISCDKNKR 101
Db 91 QQSPEDCDFKXGGLVKRCMGVTTLNQARGSPDISCDKNKR 131
RESULT 14
ABM80449
ID ABM80449 standard; protein; 170 AA.
XX
XX ABM80449;
XX
XX 18-NOV-2004 (first entry)
XX
XX Tumour-associated antigenic target (TAT) polypeptide PRO36373, SEQ.1129.
XX
XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;
XX tumour; diagnosis; cell proliferative disorder; breast cancer;
XX colorectal cancer; lung cancer; ovarian cancer; liver cancer;
XX central nervous system cancer; bladder cancer; pancreatic cancer;
XX cervical cancer; melanoma; leukaemia; hybridisation probe;
XX chromosome identification; chromosome mapping; gene mapping;
XX gene therapy; cytostatic.
XX
XX Homo sapiens.
OS
XX WO2004030615-A2.
FN
XX 15-APR-2004.
PD
XX 29-SEP-2003; 2003WO-US028547.
PF
XX 02-OCT-2002; 2002US-0414971P.
PR
XX (GETH) GENENTECH INC.
PA
XX Wu TD, Zhang Z, Zhou Y;
PI

```
XX WPI; 2004-347921/32.
DR N-PSDB; ACN37923.
XX
XX New tumor-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.
XX
XX Claim 12; SEQ ID NO 1129; 7273pp; English.
XX
XX The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acids and
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC antibodies, antagonists, binding molecules and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
XX represents a TAT polypeptide of the invention
XX
XX Sequence 170 AA;
SQ
Query Match 100.0%; Score 535; DB 8; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVLSYKEAVLRADIGINQRSSDANLYRLDLDPRPTMDGDPDTPKPSFTVKETVCPRTT 60
DB 31 QVLSYKEAVLRADIGINQRSSDANLYRLDLDPRPTMDGDPDTPKPSFTVKETVCPRTT 90
QY 61 QQSPEDCDFKKGDLVKRCMGVTTLNQARGSFDISCDKDKNR 101
DB 91 QQSPEDCDFKKGDLVKRCMGVTTLNQARGSFDISCDKDKNR 131
RESULT 15
ADW43827
ID ADW43827 standard; peptide; 170 AA.
XX
XX AC ADW43827;
XX
XX DT 24-MAR-2005 (first entry)
XX
XX DB Mouse chemerin peptide SEQ ID NO 51.
XX
XX KW gene therapy; diagnosis; cell signaling; gene therapy;
XX lymphoproliferative disease; dermatological disease; dermatological;
XX hemostatic; inflammation; antiinflammatory; hematological disease;
XX immune disorder; neoplasm; cardiovascular-gen.; cns-gen.;
XX neurological disease; hyperproliferative disorders; cytostatic; chemerin.
XX
XX OS Mus musculus.
XX
XX FN WO2005000875-A2.
XX
XX PD 06-JAN-2005.
XX
XX PF 25-JUN-2004; 2004WO-EP006945.
XX
XX PR 25-JUN-2003; 2003US-00603566.
XX
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(EURO-) EUROSREEN SA.
Wittamer V, Communi D, Dethaux M, Parmentier M, Loison C;
Ooms PDR;
WPI; 2005-058121/06.
New Chemerin polypeptides, useful for diagnosing and treating a disease,
e.g. neoplasms, hypergammaglobulinemia, paraproteinemias, purpura,
sarcoidosis, Sezary Syndrome, Waldenström's Macroglobulinemia, Gaucher's
Disease, or histiocytosis.
Example 2; SEQ ID NO 51; 183pp; English.
The invention describes a polypeptide (I) of up to 50 amino acids where
the polypeptide binds specifically to a chemerinR polypeptide. Also
described are: a nucleic acid sequence encoding (I); an expression vector
comprising the coding sequence of the nucleic acid; a transgenic animal
transfected with the expression vector; a (therapeutic) composition
comprising (I) and an isolated ChemerinR polypeptide or a nucleic acid
sequence of (I); an antibody that selectively binds to (I); identifying
an agent that modulates the interaction between a Chemerin polypeptide
and a ChemerinR polypeptide; detecting the presence, in a sample, of an
agent that modulates the interaction between a Chemerin polypeptide and a
ChemerinR polypeptide in a sample; identifying an agent that modulates
the function of ChemerinR polypeptide; detecting the presence, in a
sample, of an agent that modulates the function of ChemerinR polypeptide;
diagnosing a disease or disorder characterized by dysregulation of
ChemerinR (polypeptide) signaling; a kit, for screening agents that
modulate the signaling activity of ChemerinR polypeptide or for
diagnosing a disease or disorder characterized by dysregulation of
ChemerinR polypeptide signaling, comprising an isolated ChemerinR
polypeptide, (I), an isolated polynucleotide encoding (I), a cell
transformed with a polynucleotide encoding (I), and its packaging
materials; a non-human mammal transgenic for a Chemerin polynucleotide
encoding (I); identifying an antibody inhibiting ChemerinR activation;
and an in vitro method of inhibiting cell proliferation. The
(therapeutic) composition or expression vector is useful for preparing a
medicament for ex vivo gene therapy or for in vivo gene therapy or a
medicament for inhibiting cell proliferation, where the medicament is
used for treating a disease, e.g. neoplasms, hypergammaglobulinemia,
lymphoproliferative diseases, disorders, and/or conditions,
Macroglobulinemia, purpura, sarcoidosis, Sezary Syndrome, Waldenström's
paraproteinemia, Gaucher's Disease, histiocytosis, and any other
hyperproliferative disease. The polypeptides and polynucleotides and
methods are useful for diagnosing and treating the cited diseases. This
is the amino acid sequence of a mouse chemerin peptide used to analyse
processing of immature chemerin.
SQ Sequence 170 AA;
Query Match 100.0%; Score 535; DB 9; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVLSYKEAVLRADIGINQRSSDANLYRLDLDPRPTMDGDPDTPKPSFTVKETVCPRTT 60
DB 31 QVLSYKEAVLRADIGINQRSSDANLYRLDLDPRPTMDGDPDTPKPSFTVKETVCPRTT 90
QY 61 QQSPEDCDFKKGDLVKRCMGVTTLNQARGSFDISCDKDKNR 101
DB 91 QQSPEDCDFKKGDLVKRCMGVTTLNQARGSFDISCDKDKNR 131
Search completed: January 12, 2006, 21:48:09
Job time : 53.6679 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model
Run on: January 12, 2006, 21:43:14 ; Search time 8.94465 Seconds
(without alignments)
1086.448 Million cell updates/sec
Title: US-10-815-562-2_COPY_31_131
Perfect score: 535
Sequence: 1 QVLSYKEAVLRADGINQRS.....VTILNQARGSPDISCDKNKR 101

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 535 | 100.0 | 170 | 2 | I38932 |
| 2 | 530 | 99.1 | 170 | 2 | S74248 |
| 3 | 366 | 68.4 | 155 | 2 | S68229 |
| 4 | 361 | 67.5 | 153 | 2 | A53431 |
| 5 | 354 | 66.2 | 155 | 2 | S27018 |
| 6 | 350 | 65.4 | 172 | 2 | S68232 |
| 7 | 350 | 65.4 | 212 | 2 | S57330 |
| 8 | 347 | 64.9 | 147 | 2 | JN0900 |
| 9 | 347 | 64.9 | 149 | 2 | A53895 |
| 10 | 347 | 64.9 | 149 | 2 | S57607 |
| 11 | 347 | 64.9 | 149 | 2 | S53895 |
| 12 | 347 | 64.9 | 149 | 2 | S57609 |
| 13 | 346 | 64.7 | 228 | 2 | S40463 |
| 14 | 344 | 64.3 | 166 | 2 | S41731 |
| 15 | 343 | 64.1 | 171 | 2 | J01171 |
| 16 | 340.5 | 63.6 | 152 | 2 | S68411 |
| 17 | 340 | 63.6 | 167 | 2 | S68967 |
| 18 | 340 | 63.6 | 176 | 2 | A45328 |
| 19 | 333.5 | 62.3 | 160 | 2 | S68412 |
| 20 | 333.5 | 62.3 | 160 | 2 | S68228 |
| 21 | 327 | 61.1 | 173 | 2 | S70521 |
| 22 | 323 | 60.4 | 144 | 1 | UCL122 |
| 23 | 319 | 59.6 | 96 | 1 | XKPGC |
| 24 | 312 | 58.3 | 190 | 2 | S68230 |
| 25 | 146 | 27.3 | 135 | 2 | B46634 |
| 26 | 144 | 26.9 | 137 | 2 | A46634 |
| 27 | 85.5 | 16.0 | 200 | 2 | T46051 |
| 28 | 85 | 15.9 | 434 | 1 | KGB012 |
| 29 | 85 | 15.9 | 671 | 1 | KGB0H1 |

| | | | | | |
|----|------|------|------|---|--------|
| 30 | 84 | 15.7 | 436 | 1 | KGB0L1 |
| 31 | 84 | 15.7 | 621 | 1 | KGB0H1 |
| 32 | 79 | 14.8 | 263 | 2 | C84397 |
| 33 | 73 | 13.6 | 355 | 2 | T05390 |
| 34 | 72.5 | 13.6 | 211 | 2 | G01654 |
| 35 | 72.5 | 13.6 | 332 | 2 | S16586 |
| 36 | 71.5 | 13.4 | 364 | 2 | G82903 |
| 37 | 69.5 | 13.0 | 329 | 2 | S04132 |
| 38 | 69.5 | 13.0 | 332 | 2 | T02066 |
| 39 | 69 | 12.9 | 427 | 1 | KGH0L1 |
| 40 | 69 | 12.9 | 644 | 1 | KGH0H1 |
| 41 | 68.5 | 12.8 | 331 | 2 | T08403 |
| 42 | 68.5 | 12.8 | 1076 | 2 | JC2217 |
| 43 | 68 | 12.7 | 673 | 2 | S60177 |
| 44 | 66.5 | 12.4 | 312 | 2 | G87536 |
| 45 | 66.5 | 12.4 | 332 | 2 | S11852 |

ALIGNMENTS

RESULT 1

I38932
CAP18 precursor - human
C/Species: Homo sapiens (man)
C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C/Accession: I38932
R/Larrick, J.W.; Hirata, M.; Balint, R.F.; Lee, J.; Zhong, J.; Wright, S.C.
Infect. Immun. 63, 1291-1297, 1995
A/Title: Human CAP18, a novel antimicrobial lipopolysaccharide-binding protein.
A/Reference number: I38932; MUID:95197251; PMID:7890387
A/Accession: I38932
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-170 <RES>
A/Cross-references: UNIPROT:P49913; UNIPARC:UPI0000000A67; EMBL:U19970; NID:G643476; PID:212-130/Domain: cystatin homology <CYS>
C/Superfamily: cathelin; cystatin homology
F:212-130/Domain: cystatin homology <CYS>

Query Match 100.0%; Score 535; DB 2; Length 170;
Best Local Similarity 100.0%; Pred: No. 1.9e-50;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QVLSYKEAVLRADGINQRSNDANLYRLLDLPRTWDGDPDTPKPSFTVKETVCPRTT 60
Db 31 QVLSYKEAVLRADGINQRSNDANLYRLLDLPRTWDGDPDTPKPSFTVKETVCPRTT 90
Qy 61 QQSPEDCDPKKDGIVKRCMGTVTILNQARGSPDISCDKNKR 101
Db 91 QQSPEDCDPKKDGIVKRCMGTVTILNQARGSPDISCDKNKR 131

RESULT 2

S74248
antibacterial peptide LL-37 precursor - human
N/Alternate names: antibacterial peptide FALL39
N/Contains: antibacterial peptide LL-37; cathelin-related antibacterial peptide CAP-18
C/Species: Homo sapiens (man)
C/Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 09-Jul-2004
C/Accession: S74248; S66281; S66205; A55596; S49441; S58023
R/Gudmundsson, G.H.; Agerberth, B.; Odeberg, J.; Bergman, T.; Olsson, B.; Salcedo, R.
Eur. J. Biochem. 238, 325-332, 1996
A/Title: The human gene FALL39 and processing of the cathelin precursor to the antibacte
A/Reference number: S74248; MUID:96283824; PMID:8681941
A/Accession: S74248
A/Molecule type: DNA
A/Residues: 1-170 <GUD>
A/Cross-references: UNIPROT:P49913; UNIPARC:UPI0000017636C; EMBL:X96735
A/Accession: S78211
A/Molecule type: protein
A/Residues: 134-143 <GUS>
A/Cross-references: UNIPARC:UPI0000017636D
R/Cowland, J.B.; Johnsen, A.H.; Borregaard, N.

Best Local Similarity 67.7%; Pred. No. 6.4e-31;
Matches 65; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

QY 1 QVLSYKEAVLRAIDGINQRSDANLYRLDLDPRFTWDGDPDTPKPVSFYTKETVCPRTT 60
DB 30 QALSYLEAVLRAVDQLNEQSEPNLYRLLELDPPQDDEDPDSFKRVSFYKTVCSRTT 89

QY 61 QQSPEDCDPKKQGLVKRCMGTVTLNQRGSFDISCD 96
DB 90 QQPQCQDFKENGILLKRCGTVTLDDQVRGNFDITCN 125

RESULT 6

S68232
antimicrobial protein PR-39 precursor, cathelin-associated - pig
N;Alternate names: myeloid antibacterial protein PR-39
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 15-Feb-1997 #sequence revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S68232; JN0899; I47138; S19563
R;Zhao, C.; Ganz, T.; Lehrer, R.I.
FEBS Lett. 376, 130-134, 1995
A;Title: Structures of genes for two cathelin-associated antimicrobial peptides: prophet
A;Reference number: S68232; MUID:56105365; PMID:7498526
A;Accession: S68232
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-172 <ZHA>
A;Cross-references: UNIPROT:P80054; UNIPARC:UPI000013215A; EMBL:X89201; NID:g1165150; PID:
A;Experimental source: leukocytes
R;Storici, P.; Zanetti, M.
Biochem. Biophys. Res. Commun. 196, 1058-1065, 1993
A;Title: A cDNA derived from pig bone marrow cells predicts a sequence identical to the
A;Reference number: JN0899; MUID:94071853; PMID:8250863
A;Accession: JN0899
A;Molecule type: mRNA
A;Residues: 1-20, 'A', 22-172 <STO>
A;Cross-references: UNIPARC:UPI000016C6E7; GB:I23825; NID:g435100; PIDN:AAA31109.1; PID:
A;Experimental source: bone marrow cells
R;Gudmundson, G.H.; Magnusson, K.P.; Chowdhary, B.P.; Johansson, M.; Andersson, L.; Bor
proc. Natl. Acad. Sci. U.S.A. 92, 7085-7089, 1995
A;Title: Structure of the gene for porcine peptide antibiotic PR-39, a cathelin gene fam
A;Reference number: I47138; MUID:95350216; PMID:7624374
A;Accession: I47138
A;Status: preliminary; translated from GB/EMBL/DBEJ
A;Molecule type: DNA
A;Residues: 1-28, 'T', 30-89, 'QR', 92-116, 'NDP', 120-172 <GUD>
A;Cross-references: UNIPARC:UPI000016C6AC; EMBL:X87236; NID:g829142; PIDN:CAA60682.1; PT
R;Agerberth, B.; Lee, J.Y.; Bergman, T.; Carlquist, M.; Boman, H.G.; Mutt, V.; Joernvall
Eur. J. Biochem. 202, 849-854, 1991
A;Title: Amino acid sequence of PR-39. Isolation from pig intestine of a new member of t
A;Reference number: S19563; MUID:92111534; PMID:1765098
A;Accession: S19563
A;Molecule type: protein
A;Residues: 131-169 <AGE>
A;Cross-references: UNIPARC:UPI000002D613
A;Experimental source: intestine
C;Genetics:
A;Gene: PR39
A;Introns: 66/3; 102/3; 126/3
C;Superfamily: cathelin; cystatin homology
C;Keywords: amidated carboxyl end; antibacterial
P;1-29/Domain: signal sequence #status predicted <SIG>
P;22-129/Domain: cystatin homology <CVS>
P;130-130/Domain: propeptide #status predicted <PRO>
P;131-169/Product: antimicrobial protein PR-39 #status experimental <MAT>
P;169/Modified site: amidated carboxyl end (Pro) (amide in mature form from following 91

Query Match 65.4%; Score 350; DB 2; Length 172;
Best Local Similarity 68.0%; Pred. No. 1.9e-30;
Matches 66; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 1 QVLSYKEAVLRAIDGINQRSDANLYRLDLDPRFTWDGDPDTPKPVSFYTKETVCPRTT 60

A;Title: Protegrins: leukocyte antimicrobial peptides that combine features of corticost
A;Reference number: S34585; MUID:93327946; PMID:8335113
A;Accession: S34586
A;Molecule type: protein
A;Residues: 131-146 <KOK>
A;Cross-references: UNIPARC:UPI000014310F
C;Comment: This protein plays a role in the nonoxidative antimicrobial defense mechanism
C;Superfamily: cathelin; cystatin homology
C;Keywords: amidated carboxyl end; antibacterial; neutrophil
F;1-29/Domain: signal sequence #status predicted <SIG>
F;22-129/Domain: cystatin homology <CYS>
F;131-146/Product: protegrin 2 #status experimental <MAT>
F;146/Modified site: amidated carboxyl end (Val) (amide in mature form from following gl

Query Match 64.9%; Score 347; DB 2; Length 147;
Best Local Similarity 66.0%; Pred. No. 3.4e-30;
Matches 64; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

Qy 1 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLPRTWDGDPDTPKPVSTTKETVCPRTT 60
Db 30 QALSRYEAVLRAVDRLNEQSEANLYRLLELDQPPKADEDPTGTPKPVSTTKETVCPRPT 89

Qy 61 QQSPEDCDFKQGLVKRCMGVTTLNQARGSPDISCDK 97
Db 90 RQPELCDFKENGVRKQCVGTTLQDKPDLDTCNE 126

RESULT 9
A53895
protegrin 3 precursor - pig
N;Alternate names: neutrophil peptide 2
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 01-Dec-1995 #sequence revision 01-Dec-1995 #text_change 09-Jul-2004
C;Accession: S66285; A53895; S34587; S36821; S57608
R;Zhao, C.; Ganz, T.; Lehrer, R.I.
FEBS Lett. 368, 197-202, 1995
A;Title: The structure of porcine protegrin genes.
A;Reference number: S66283; MUID:95354835; PMID:7628604
A;Accession: S66285
A;Molecule type: DNA
A;Residues: 1-149 <ZHA>
A;Cross-references: UNIPROT:P32196; UNIPARC:UPI0000131777; EMBL:X84095; NID:G987644; PID:
R;Zhao, C.; Liu, L.; Lehrer, R.I.
FEBS Lett. 346, 285-288, 1994
A;Title: Identification of a new member of the protegrin family by cDNA cloning.
A;Reference number: S45712; MUID:94283613; PMID:8013647
A;Accession: A53895
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-149 <ZHA>
A;Cross-references: UNIPARC:UPI0000131777; GB:X83267; NID:G603037; PIDN:CAA58240.1; PID:
R;Kokryakov, V.N.; Harwig, S.S.L.; Panyutich, E.A.; Abdalla, K.O.M.A.; Chernushevich, I.V.; Egorov,
FEBS Lett. 327, 231-236, 1993
A;Title: Protegrins: leukocyte antimicrobial peptides that combine features of corticost
A;Reference number: S34585; MUID:93327946; PMID:8335113
A;Accession: S34587
A;Molecule type: protein
A;Residues: 131-148 <KOK>
A;Cross-references: UNIPARC:UPI0000143110
R;Mirgorodskaya, O.A.; Shevchenko, A.A.; Abdalla, K.O.M.A.; Chernushevich, I.V.; Egorov,
FEBS Lett. 330, 339-342, 1993
A;Title: Primary structure of three cationic peptides from porcine neutrophils. Sequence
A;Reference number: S36820; MUID:93387466; PMID:8375505
A;Accession: S36821
A;Molecule type: protein
A;Residues: 131-148 <KOK>
A;Cross-references: UNIPARC:UPI0000143110
C;Genetics:
A;Gene: NPG3
A;Introns: 66/3; 102/3; 126/3
C;Superfamily: cathelin; cystatin homology
C;Keywords: amidated carboxyl end; antibacterial; neutrophil
F;1-29/Domain: signal sequence #status predicted <SIG>

F;22-129/Domain: cystatin homology <CYS>
F;30-130/Domain: propeptide #status predicted <PRO>
F;131-148/Product: protegrin 3 #status experimental <MAT>
F;148/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gl

Query Match 64.9%; Score 347; DB 2; Length 149;
Best Local Similarity 66.0%; Pred. No. 3.5e-30;
Matches 64; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

Qy 1 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLPRTWDGDPDTPKPVSTTKETVCPRTT 60
Db 30 QALSRYEAVLRAVDRLNEQSEANLYRLLELDQPPKADEDPTGTPKPVSTTKETVCPRPT 89

Qy 61 QQSPEDCDFKQGLVKRCMGVTTLNQARGSPDISCDK 97
Db 90 RQPELCDFKENGVRKQCVGTTLQDKPDLDTCNE 126

RESULT 10
S57607
protegrin 1 precursor - pig
N;Alternate names: neutrophil peptide 1
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Oct-1995 #sequence revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S66284; S45712; S36820; S34585; S57607
R;Zhao, C.; Ganz, T.; Lehrer, R.I.
FEBS Lett. 368, 197-202, 1995
A;Title: The structure of porcine protegrin genes.
A;Reference number: S66283; MUID:95354835; PMID:7628604
A;Accession: S66284
A;Molecule type: DNA
A;Residues: 1-149 <ZHA>
A;Cross-references: UNIPROT:P32194; UNIPARC:UPI0000131775; EMBL:X84094; NID:G987642; PID:
R;Zhao, C.; Liu, L.; Lehrer, R.I.
FEBS Lett. 346, 285-288, 1994
A;Title: Identification of a new member of the protegrin family by cDNA cloning.
A;Reference number: S45712; MUID:94283613; PMID:8013647
A;Accession: S45712
A;Molecule type: mRNA
A;Residues: 1-149 <ZHA>
A;Cross-references: UNIPARC:UPI0000131775; GB:X79868; NID:G603035; PIDN:CAA56251.1; PID:
R;Mirgorodskaya, O.A.; Shevchenko, A.A.; Abdalla, K.O.M.A.; Chernushevich, I.V.; Egorov,
FEBS Lett. 330, 339-342, 1993
A;Title: Primary structure of three cationic peptides from porcine neutrophils. Sequence
A;Reference number: S36820; MUID:93387466; PMID:8375505
A;Accession: S36820
A;Molecule type: protein
A;Residues: 131-148 <KOK>
A;Cross-references: UNIPARC:UPI0000034C2E
C;Genetics:
A;Gene: NPG1
A;Introns: 66/3; 102/3; 126/3
C;Superfamily: cathelin; cystatin homology
C;Keywords: amidated carboxyl end; antibacterial; neutrophil
F;1-29/Domain: signal sequence #status predicted <SIG>
F;22-129/Domain: cystatin homology <CYS>
F;30-130/Domain: propeptide #status predicted <PRO>
F;131-148/Product: protegrin 1 #status experimental <MAT>
F;148/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gl;

Query Match 64.9%; Score 347; DB 2; Length 149;
Best Local Similarity 66.0%; Pred. No. 3.5e-30;
Matches 64; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

Qy 1 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLPRTWDGDPDTPKPVSTTKETVCPRTT 60

Db 30 QALSRYEAVLRADVRLNEQSSSEANLYRLLELDLPKPADEDPGTPKPVSVFTVKETVCPRTT 89
Qy 61 QQSPEDCDFKKGGLVKRCMGTVTLNQARGSFSDISCDK 97
Db 90 RQPELCDFKENGVRKQCVGTITLDQIKDPLDITCNE 126

RESULT 11

B53895
protegrin 4 precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C:Accession: B53895
R:Zhao, C.; Liu, L.; Lehrer, R.I.
FEBS Lett. 346, 285-288, 1994
A>Title: Identification of a new member of the protegrin family by cDNA cloning.
A:Reference number: S45712; MUID:94283613; PMID:8013647
A:Accession: B53895
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-149 <ZHA>
A:Cross-references: UNIPROT:P49933; UNIPARC:UPI0000131778; GB:X83268; NID:G603039; PIDN:
C:Superfamily: cathelin; cystatin homology
C:Keywords: amidated carboxyl end; antibacterial; neutrophil
F;1-29/Domain: signal sequence #status predicted <SIG>
F;22-129/Domain: cystatin homology <CYS>
F;131-148/Product: protegrin 4 #status predicted <MAT>
F;148/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gl

Query Match 64.9%; Score 347; DB 2; Length 149;
Best Local Similarity 66.0%; Pred. No. 3.5e-30;
Matches 64; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

Qy 1 QVLSYKEAVLRADVRLNEQSSSEANLYRLLELDLPKPADEDPGTPKPVSVFTVKETVCPRTT 60
Db 30 QALSRYEAVLRADVRLNEQSSSEANLYRLLELDLPKPADEDPGTPKPVSVFTVKETVCPRTT 89

Qy 61 QQSPEDCDFKKGGLVKRCMGTVTLNQARGSFSDISCDK 97
Db 90 RQPELCDFKENGVRKQCVGTITLDQIKDPLDITCNE 126

RESULT 12

S57609
protegrin 5 precursor - pig
N:Alternate names: cathelin-associated antimicrobial peptide
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C:Accession: S66283; S57609
R:Zhao, C.; Ganz, T.; Lehrer, R.I.
FEBS Lett. 368, 197-202, 1995
A>Title: The structure of porcine protegrin genes.
A:Reference number: S66283; MUID:95354835; PMID:7628604
A:Accession: S66283
A:Molecule type: DNA
A:Residues: 1-149 <ZHA>
A:Cross-references: UNIPROT:P49934; UNIPARC:UPI0000131779; EMBL:X84096; NID:G887646; PID

A:Experimental source: leukocytes
C:Genetics:
A:Gene: NPG5
A:Introns: 66/3; 102/3; 126/3
C:Superfamily: cathelin; cystatin homology
C:Keywords: amidated carboxyl end; antibacterial
F;1-29/Domain: signal sequence #status predicted <SIG>
F;22-129/Domain: cystatin homology <CYS>
F;30-130/Domain: propeptide #status predicted <PRO>
F;131-148/Product: protegrin 5 #status predicted <MAT>
F;148/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gl

Query Match 64.9%; Score 347; DB 2; Length 149;
Best Local Similarity 66.0%; Pred. No. 3.5e-30;
Matches 64; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

Qy 1 QVLSYKEAVLRADVRLNEQSSSEANLYRLLELDLPKPADEDPGTPKPVSVFTVKETVCPRTT 60
Db 30 QALSRYEAVLRADVRLNEQSSSEANLYRLLELDLPKPADEDPGTPKPVSVFTVKETVCPRTT 89
Qy 61 QQSPEDCDFKKGGLVKRCMGTVTLNQARGSFSDISCDK 97
Db 90 RQPELCDFKENGVRKQCVGTITLDQIKDPLDITCNE 126

RESULT 13

S40463
prophenin (PF-2) precursor - pig
N:Alternate names: antimicrobial peptide; cathelin-like antibacterial peptide precursor
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S40463; S57331; S68233
R:Pungercar, J.; Strukelj, B.; Kopitar, G.; Renko, M.; Lenarcic, B.; Gubensek, F.; Turk, FEBS Lett. 336, 284-288, 1993
A>Title: Molecular cloning of a putative homolog of proline/arginine-rich antibacterial
A:Reference number: S40463; MUID:94085623; PMID:8262247
A:Accession: S40463
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-228 <PUN>
A:Cross-references: UNIPROT:PS1525; UNIPARC:UPI0000131713; EMBL:X75438; NID:G443812; PID
R:Strukelj, B.; Pungercar, J.; Kopitar, G.; Renko, M.; Lenarcic, B.; Berbic, S.; Turk, Biol. Chem. Hoppe-Seyler 376, 507-510, 1995
A>Title: Molecular cloning and identification of a novel porcine cathelin-like antibacte
A:Reference number: S57330; MUID:96042752; PMID:7576250
A:Accession: S57331
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-228 <STR>
A:Cross-references: UNIPARC:UPI0000131713
R:Zhao, C.; Ganz, T.; Lehrer, R.I.
FEBS Lett. 376, 130-134, 1995
A>Title: Structures of genes for two cathelin-associated antimicrobial peptides: prophen

A:Reference number: S68232; MUID:96105365; PMID:7498526
A:Accession: S68233
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-228 <ZHA>
A:Cross-references: UNIPARC:UPI0000131713; EMBL:X89202; NID:G1165148; PIDN:CAA61488.1; P

A:Introns: 66/3; 102/3; 126/3
C:Superfamily: cathelin; cystatin homology
F;1-29/Domain: signal sequence #status predicted <SIG>
F;22-129/Domain: cystatin homology <CYS>
F;30-228/Product: prophenin (PF-2) #status predicted <MAT>
Query Match 64.7%; Score 346; DB 2; Length 228;
Best Local Similarity 63.4%; Pred. No. 7.1e-30;
Matches 64; Conservative 19; Mismatches 18; Indels 0; Gaps 0;

Qy 1 QVLSYKEAVLRADVRLNEQSSSEANLYRLLELDLPKPADEDPGTPKPVSVFTVKETVCPRTT 60
Db 30 QALSRYEAVLRADVRLNEQSSSEANLYRLLELDLPKPADEDPGTPKPVSVFTVKETVCPRTT 89

Qy 61 QQSPEDCDFKKGGLVKRCMGTVTLNQARGSFSDISCDK 101
Db 90 RQPELCDFKENGVRKQCVGTITLDQIKDPLDITCNEGVRR 130

RESULT 14

S41731
antibacterial protein precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S41731
R:Storici, P.; Scocchi, M.; Tossi, A.; Gennaro, R.; Zanetti, M.
FEBS Lett. 337, 303-307, 1994
A>Title: Chemical synthesis and biological activity of a novel antibacterial peptide ded

Query Match 64.7%; Score 346; DB 2; Length 228;
Best Local Similarity 63.4%; Pred. No. 7.1e-30;
Matches 64; Conservative 19; Mismatches 18; Indels 0; Gaps 0;

Qy 1 QVLSYKEAVLRADVRLNEQSSSEANLYRLLELDLPKPADEDPGTPKPVSVFTVKETVCPRTT 60
Db 30 QALSRYEAVLRADVRLNEQSSSEANLYRLLELDLPKPADEDPGTPKPVSVFTVKETVCPRTT 89

Qy 61 QQSPEDCDFKKGGLVKRCMGTVTLNQARGSFSDISCDK 101
Db 90 RQPELCDFKENGVRKQCVGTITLDQIKDPLDITCNEGVRR 130

RESULT 14

S41731
antibacterial protein precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S41731
R:Storici, P.; Scocchi, M.; Tossi, A.; Gennaro, R.; Zanetti, M.
FEBS Lett. 337, 303-307, 1994
A>Title: Chemical synthesis and biological activity of a novel antibacterial peptide ded

Query Match 64.9%; Score 347; DB 2; Length 149;
Best Local Similarity 66.0%; Pred. No. 3.5e-30;
Matches 64; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

Search completed: January 12, 2006, 21:51:07
Job time : 8.94465 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 12, 2006, 21:42:24 ; Search time 49.1956 Seconds
(without alignments)
1448.471 Million cell updates/sec

Title: US-10-815-562-2_COPY_31_131
Perfect score: 535
Sequence: 1 QVLSYKEAVLRADIGNRS.....VTLNQARGSFDISCDKNR 101

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot.05.80.*
1: uniprot_eprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------------|---------------------|
| 1 | 535 | 100.0 | 170 | 1 FAL39 HUMAN | P49913 homo sapien |
| 2 | 535 | 100.0 | 170 | 1 FAL39 MACMU | Q71893 macaca mula |
| 3 | 503 | 94.0 | 170 | 2 Q9GLV5 MACMU | Q9GLV5 macaca mula |
| 4 | 401 | 75.0 | 157 | 2 O62841 HORSE | O62841 equus caball |
| 5 | 367 | 68.6 | 170 | 2 O62842 HORSE | O62842 equus caball |
| 6 | 366 | 68.4 | 155 | 1 BCTN1 SHEEP | P54230 ovis aries |
| 7 | 364 | 68.0 | 156 | 2 O62840 HORSE | O62840 equus caball |
| 8 | 361 | 67.5 | 153 | 1 PMP23 PIG | P49930 sus scrofa |
| 9 | 361 | 67.5 | 176 | 1 BCTN5 SHEEP | P79362 ovis aries |
| 10 | 361 | 67.5 | 176 | 2 BCTN5 SHEEP | P79362 ovis aries |
| 11 | 361 | 67.5 | 176 | 2 O4JFB9 CAPRI | O4JFB9 capra hircu |
| 12 | 354 | 66.2 | 155 | 1 BCTN1 BOVIN | P22226 bos taurus |
| 13 | 352.5 | 65.9 | 159 | 1 BMA28 BOVIN | P54229 bos taurus |
| 14 | 350 | 65.4 | 172 | 1 PR39 PIG | P80054 sus scrofa |
| 15 | 350 | 65.4 | 212 | 1 PF11 PIG | P51524 sus scrofa |
| 16 | 347 | 64.9 | 147 | 1 PG2 PIG | P32195 sus scrofa |
| 17 | 347 | 64.9 | 149 | 1 PG1 PIG | P32194 sus scrofa |
| 18 | 347 | 64.9 | 149 | 1 PG3 PIG | P32196 sus scrofa |
| 19 | 347 | 64.9 | 149 | 1 PG4 PIG | P49933 sus scrofa |
| 20 | 347 | 64.9 | 149 | 1 PG5 PIG | P49934 sus scrofa |
| 21 | 346 | 64.7 | 228 | 1 PF21 PIG | P51525 sus scrofa |
| 22 | 344 | 64.3 | 166 | 1 PMP35 PIG | P49931 sus scrofa |
| 23 | 344 | 64.3 | 171 | 2 Q71KMS RAT | Q71KMS rattus norv |
| 24 | 343 | 64.1 | 171 | 1 CAP18 RABIT | P25230 coryctolagus |
| 25 | 340.5 | 63.6 | 160 | 1 SC51 SHEEP | P49928 ovis aries |
| 26 | 340 | 63.6 | 167 | 1 PMP37 PIG | P49932 sus scrofa |
| 27 | 340 | 63.6 | 176 | 1 BCTN5 BOVIN | P196620 bos taurus |
| 28 | 339.5 | 63.5 | 165 | 1 BMA34 BOVIN | P56425 bos taurus |
| 29 | 338.5 | 63.3 | 158 | 1 BMA27 BOVIN | P54228 bos taurus |
| 30 | 334 | 62.4 | 158 | 2 Q9XSQB CAPRI | Q9XSQB capra hircu |
| 31 | 333.5 | 62.3 | 160 | 1 SC52 SHEEP | P49929 ovis aries |

| | | | | | |
|----|-------|------|-----|----------------|--------------------|
| 32 | 333 | 62.2 | 190 | 1 BCTN7 BOVIN | P19661 bos taurus |
| 33 | 332 | 62.1 | 172 | 2 Q6TN20 CANFA | Q6TN20 canis famil |
| 34 | 327 | 61.1 | 173 | 1 CRAMP MOUSE | P51437 mus musculu |
| 35 | 324 | 60.6 | 144 | 2 Q683R8 BUBBU | Q683R8 bubalus bub |
| 36 | 323 | 60.4 | 144 | 1 INDC BOVIN | P33046 bos taurus |
| 37 | 319 | 59.6 | 96 | 1 ICTL PIG | P15175 sus scrofa |
| 38 | 318 | 59.4 | 164 | 2 P79361 SHEEP | P79361 ovis aries |
| 39 | 318 | 59.4 | 190 | 2 Q9XSQB CAPRI | Q9XSQB capra hircu |
| 40 | 316 | 59.1 | 165 | 2 P79360 SHEEP | P79360 ovis aries |
| 41 | 312 | 58.3 | 190 | 1 BCTN7 SHEEP | P50415 ovis aries |
| 42 | 308 | 57.6 | 224 | 2 O19031 SHEEP | O19031 ovis aries |
| 43 | 303.5 | 56.7 | 165 | 2 P82017 CAPRI | P82017 capra hircu |
| 44 | 299 | 55.9 | 182 | 2 O19040 SHEEP | O19040 ovis aries |
| 45 | 280.5 | 52.4 | 178 | 2 Q91X12 CAVPO | Q91X12 cavia porce |

ALIGNMENTS

RESULT 1
FAL39 HUMAN
ID FAL39_HUMAN STANDARD; PRT; 170 AA.
AC P49913;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Antibacterial protein FAL39 precursor (FALL-39 peptide antibiotic)
DE (Cationic antimicrobial protein CAP-18) (hCAP-18) (HSD26) [Contains:
DE Antibacterial protein LL-37].
GN Name=CAMP; Synonyms=CAP18, FALL39;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE [MRNA], AND SYNTHESIS OF 132-170.
RC TISSUE=Bone marrow;
RX MEDLINE=95116523; PubMed=7529412;
RA Agerberth B., Gunne H., Odeberg J., Kogner P., Boman H.G.,
RA Gudmundsson G.H.;
RT "FALL-39, a putative human peptide antibiotic, is cysteine-free and
RT expressed in bone marrow and testis.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:195-199 (1995).
[2]
RP NUCLEOTIDE SEQUENCE [MRNA], AND PROTEIN SEQUENCE OF 42-68 AND 83-100.
RC TISSUE=Bone marrow;
RX MEDLINE=95339969; PubMed=7615076; DOI=10.1016/0014-5793(95)00634-L;
RA Cowland J.B., Johnsen A.H., Borregaard N.;
RA "hCAP-18, a cathelin/pro-bactenecin-like protein of human neutrophil
RT specific granules.";
RL FEBS Lett. 368:173-176 (1995).
[3]
RN [3]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Bone marrow;
RX MEDLINE=95197251; PubMed=7890387;
RA Larrick J.W., Hirata M., Balint R.F., Lee J., Zhong J., Wright S.C.;
RA "Human CAP18: a novel antimicrobial lipopolysaccharide-binding
RT protein.";
RL Infect. Immun. 63:1291-1297 (1995).
[4]
RN [4]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=97102716; PubMed=8946956; DOI=10.1016/S0014-5793(96)01199-4;
RA Larrick J.W., Lee J., Ma S., Li X., Francke U., Wright S.C.,
RA Balint R.F.;
RT "Structural, functional analysis and localization of the human CAP18
RT gene.";
RL FEBS Lett. 398:74-80 (1996).
[5]
RN [5]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX PubMed=8681941;
RA Gudmundsson G.H., Agerberth B., Odeberg J., Bergman T., Olsson B.,
RA Salcedo R.;

Ref 1-4 Ref

"The human gene FALL39 and processing of the cathelin precursor to the antibacterial peptide LL-37 in granulocytes."; Eur. J. Biochem. 238:325-332(1996).

[6]

RP NUCLEOTIDE SEQUENCE [MRNA].
RA Gao Y., Huang Y.F., Xia X.Y.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.

[7]

RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Testis;
RA Wu N., Miao S.Y., Zhang X.D., Qiao Y., Liang G., Wang L.F.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.

[8]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA Halleck A., Ebert L., Moundinya M., Schick M., Eisenstein S.,
RA Heubert P., Ketrang K., Schatten R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., LaBaer J.;
RL "Cloning of human full open reading frames in Gateway(TM) system entry vector (pDONR201).";
RT Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

[9]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.C., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J.J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -!- FUNCTION: Binds to bacterial lipopolysaccharides (LPS), has antibacterial activity.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Expressed in bone marrow and testis and neutrophils.

CC -!- PTM: The N-terminus is blocked.

CC -!- SIMILARITY: Belongs to the cathelicidin family.

CC

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DR EMBL; Z38026; CAAB6115.1; -; mRNA.
DR EMBL; X89658; CAAG1805.1; -; mRNA.
DR EMBL; U19970; AAG74084.1; -; mRNA.
DR EMBL; U48795; AAC02634.1; -; Genomic DNA.
DR EMBL; X96735; -; NOT ANNOTATED CDS; Genomic DNA.
DR EMBL; AY162210; AAN78318.1; -; mRNA.
DR EMBL; AY251531; AAP20054.1; -; mRNA.
DR EMBL; CR457083; CAG33364.1; -; mRNA.
DR EMBL; CR541961; CAG46759.1; -; mRNA.
DR EMBL; BC055085; AAH55089.1; -; mRNA.
DR F01; I38932; I38932.
DR F01; S74248; S74248.
DR HSP; P32196; 1KW1.
DR Ensembl; ENSG00000164047; Homo sapiens.

DR HGNC; HGNC:1472; CAMP.
DR MIM; 600474; -.
DR GO; GO:0042742; P:defense response to bacteria; TAS.
DR InterPro; IPR001894; Cathelicidin.
DR PANTHER; PTHR10206; Cathelicidin; 1.
DR Pfam; PF00666; Cathelicidins; 1.
DR ProDom; PD001838; Cathelicidin; 1.
DR PROSITE; PS00946; CATHELICIDINS_1; 1.
DR PROSITE; PS00947; CATHELICIDINS_2; 1.
DR Antibiotic; Antimicrobial; Direct protein sequencing;
KW Pyrolydione carboxylic acid; Signal.
FT SIGNAL 1 30
FT PROPEP 31 131
FT CHAIN 132 170
FT CHAIN 134 170
FT MOD_RES 31 31
FT DISULFID 86 97
FT DISULFID 108 125
FT CONFLICT 6
FT SEQUENCE 170 AA; 19301 MW; 055B07DCA95A7D16 CRC64;
SQ
Query Match 100.0%; Score 535; DB 1; Length 170;
Best Local Similarity 100.0%; Pred. No. 7e-49;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVLSYKEAVLRADIGINORSSDANLYRLLDLPRTMDGDDPTPKPVSTVKETVCPRTT 60
DB 31 QVLSYKEAVLRADIGINORSSDANLYRLLDLPRTMDGDDPTPKPVSTVKETVCPRTT 90
QY 61 QQSPEDCDFFKDGVLKRCMGVTTLNQARGSFDISCDKNKR 101
DB 91 QQSPEDCDFFKDGVLKRCMGVTTLNQARGSFDISCDKNKR 131
RESULT 2
FALL39 MACMU STANDARD; PRT; 170 AA.
ID FALL39 MACMU
AC Q715N3;
DC 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Antibacterial protein FALL-39 precursor (FALL-39 peptide antibiotic)
DE (Cationic antimicrobial protein CAP-18) (rhCAP-18) [Contains:
DE Antibacterial protein LL-37 (rLL-37)].
GN Name=CAMP; Synonyms=CAP18, FALL39;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopitheidae; Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA], AND TISSUE SPECIFICITY.
RX MEDLINE=21137962; PubMed=11238224; DOI=10.1128/CDLI.8.2.370-375.2001;
RA Bals R., Lang C., Weiner D.J., Vogelmeier C., Welsch U., Wilson J.M.;
RT "Rhesus monkey (Macaca mulatta) mucosal antimicrobial peptides are close homologues of human molecules";
RL Clin. Diagn. Immunol. 8:370-375(2001).
CC -!- FUNCTION: Binds to bacterial lipopolysaccharides (LPS), has antibacterial activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed in epithelia of various organs. Most abundant peptide levels are found in organs lining outer or inner body surfaces, such as organs of the respiratory or gastrointestinal tract.
CC -!- SIMILARITY: Belongs to the cathelicidin family.
CC
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Db 91 QKSPEDCDPKFDGLVKRCVGTVLNQARDFDISCDKNRR 131

RESULT 4

O62841_HORSE

ID O62841_HORSE PRELIMINARY; PRT; 157 AA.

AC O62841; 157

DT 01-AUG-1998 (T-EMBLrel. 07, Created)

DT 01-AUG-1998 (T-EMBLrel. 07, Last sequence update)

DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)

DE Myeloid cathelicidin 2 precursor.

GN Name=eCATH-2;

OS Equus caballus (Horse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Perissodactylia; Equidae; Equus.

OX NCBI_TaxID=9796;

[1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Bone marrow;

RC MEDLINE=99402973; PubMed=10471829; DOI=10.1016/S0014-5793(99)01097-2;

RA Scocchi M., Bontempo D., Boscolo S., Tomasinsig L., Giulotto E., Zanetti M.;

RT "Novel cathelicidins in horse leukocytes.";

RL FEBS Lett. 457:459-464(1999).

DR EMBL; AJ224928; CAAL227.1; -, mRNA.

DR HSSP; P32196; IKWI.

DR SWR; O62841; 30-130.

DR CO; GO:0005576; C:extracellular region; IEA.

DR GO; GO:0006952; P:defense response; IEA.

DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.

DR InterPro; IPR001894; Cathelicidin.

DR Pfam; PF006666; Cathelicidins; 1.

DR ProDom; PS001838; Cathelicidin; 1.

DR PROSITE; PS00946; CATHELICIDINS_1; 1.

DR PROSITE; PS00947; CATHELICIDINS_2; 1.

KW Signal.

FT SIGNAL 1 29 Potential.

FT CHAIN 30 157 myeloid cathelicidin 2.

SQ SEQUENCE 157 AA; 18153 MW; 142C493D2B307CC CRC64;

Query Match 75.0%; Score 401; DB 2; Length 157;

Best Local Similarity 77.3%; Pred. No. 1.3e-34;

Matches 75; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

Qy 1 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLPRTMDGPDTPKPSFTVKETVCPRTT 60

Db 30 QTL-SYKEAVLRAVDGLNQSSDNLRYLLLELPLPKEDPDTPKPSFTVKETVCPRTT 89

Qy 61 QQSPEDCDPKFDGLVKRCVGTVLNQARDFDISCDK 97

Db 90 QQPLEECDPKFENGLVKQCVGTVVLDPKAFYDISCDK 126

RESULT 5

O62842_HORSE

ID O62842_HORSE PRELIMINARY; PRT; 170 AA.

AC O62842; 170

DT 01-AUG-1998 (T-EMBLrel. 07, Created)

DT 01-AUG-1998 (T-EMBLrel. 07, Last sequence update)

DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)

DE Myeloid cathelicidin 3 precursor.

GN Name=eCATH-3;

OS Equus caballus (Horse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Perissodactylia; Equidae; Equus.

OX NCBI_TaxID=9796;

[1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Bone marrow;

RC MEDLINE=99402973; PubMed=10471829; DOI=10.1016/S0014-5793(99)01097-2;

RA Scocchi M., Bontempo D., Boscolo S., Tomasinsig L., Giulotto E., Zanetti M.;

RT "Novel cathelicidins in horse leukocytes.";

```
RL FEBS Lett. 457:459-464(1999).
DR EMBL; AJ224929; CAA12228.1; -; mRNA.
DR HSSP; P32196; 1KWI.
DR SNR; O62842; 30-130.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
DR InterPro; IPR001894; Cathelicidin.
DR Pfam; PF00666; Cathelicidin; 1.
DR PROSITE; PS00946; CATHLICIDINS_1; 1.
DR PROSITE; PS00947; CATHLICIDINS_2; 1.
DR SIGNAL.
FT SIGNAL 1 29 Potential.
FT CHAIN 30 170 myeloid cathelicidin 3.
SQ SEQUENCE 170 AA; 19299 MW; 5C35F1FA2D112BC8 CRC64;

Query Match 68.6%; Score 367; DB 2; Length 170;
Best Local Similarity 68.0%; Pred. No. 5.9e-31;
Matches 68; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

QY 1 QVLSYKEAVLRADGINQRSSDANLYRLDLPRTMDGDPDPKPVSVFTVKETVCPRTT 60
Db 30 QALSKEAVLRADVGLNQRSSDANLYRLDLPKGDSDTPKPVSVFMVKETVCPRTM 89

QY 61 QQSPEDCDFKDGKGLVKRCMGTVTLNQARSGFDISCDKNK 100
Db 90 KQTPEQCDPFKENGKLVQCVCVTILDVPKQYFDASCDPEQR 129

RESULT 6
BCTN1_SHEEP STANDARD; PRT; 155 AA.
ID BCTN1_SHEEP
AC F54230;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Cyclic dodecapeptide precursor (Bactenecin 1) (Bac1).
GN Names=BAC1A; Synonyms=BODEN;
GN and
GN Names=BAC1B; Synonyms=BODEB;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Bone marrow.
RX MEDLINE=96105386; PubMed=7498547; DOI=10.1016/0014-5793(95)01285-3;
RA Bagella L., Scocchi M., Zanetti M.;
RT "cDNA sequences of three sheep myeloid cathelicidins.";
RL FEBS Lett. 376:225-228(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC TISSUE=Liver;
RX MEDLINE=98121317; PubMed=9461419; DOI=10.1016/S0378-1119(97)00569-6;
RA Huttner K.M., Lambeth M.R., Burkin H.R., Broad T.E.;
RT "Localization and genomic organization of sheep antimicrobial peptides genes.";
RL Gene 206:85-91(1998).
CC -1- FUNCTION: Potent microbicidal activity, active against
CC Staphylococcus aureus and Escherichia coli (By similarity).
CC -1- SIMILARITY: Belongs to the cathelicidin family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; L46853; AAA85469.1; -; mRNA.
DR EMBL; U60595; AAB49710.1; -; Genomic_DNA.
```

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DR EMBL; U60596; AAB49711.1; -; Genomic_DNA.
DR PIR; S68229; S68229.
DR HSSP; P32196; 1KWI.
DR SNR; P54230; 30-130.
DR InterPro; IPR001894; Cathelicidin.
DR PANTHER; PTHR10206; Cathelicidin; 1.
DR Pfam; PF00666; Cathelicidin; 1.
DR ProDom; PD001838; Cathelicidin; 1.
DR PROSITE; PS00946; CATHLICIDINS_1; 1.
DR PROSITE; PS00947; CATHLICIDINS_2; 1.
DR Antibiotic; Antimicrobial; Pyrrolidone carboxylic acid; Signal.
FT SIGNAL 1 29 Potential.
FT PROPEP 30 143 By similarity.
FT PEPTIDE 144 155 Cyclic dodecapeptide.
FT MOD_RES 30 30 Pyrrolidone carboxylic acid (By
FT similarity).
FT DISULFID 85 96 By similarity.
FT DISULFID 107 124 By similarity.
FT DISULFID 146 154 By similarity.
SQ SEQUENCE 155 AA; 17648 MW; 1690638C791B1736 CRC64;

Query Match 68.4%; Score 366; DB 1; Length 155;
Best Local Similarity 69.8%; Pred. No. 6.8e-31;
Matches 67; Conservative 16; Mismatches 13; Indels 0; Gaps 0;

QY 1 QVLSYKEAVLRADGINQRSSDANLYRLDLPRTMDGDPDPKPVSVFTVKETVCPRTT 60
Db 30 QVLSYKEAVLRADVQLNEQSSEPNYRLLELOPQDDPDSPKRVSVFVKETVCPRTT 89

QY 61 QQSPEDCDFKDGKGLVKRCMGTVTLNQARSGFDISCD 96
Db 90 QQPPEQCDPFKENGKLVKRCMGTVTLDOVRGNFDITCN 125

RESULT 7
O62840 HORSE
ID O62840 HORSE PRELIMINARY; PRT; 156 AA.
AC O62840;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Myeloid cathelicidin 1 precursor.
GN Name=eCATH-1;
GN Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Bone marrow.
RX MEDLINE=99402973; PubMed=10471829; DOI=10.1016/S0014-5793(99)01097-2;
RA Scocchi M., Bontempo D., Boscolo S., Tomasinsig L., Giulotto E.,
RA Zanetti M.;
RT "Novel cathelicidins in horse leukocytes.";
RL FEBS Lett. 457:459-464(1999).
DR EMBL; AJ224927; CAA12226.1; -; mRNA.
DR HSSP; P32196; 1KWI.
DR SNR; O62840; 30-130.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
DR InterPro; IPR001894; Cathelicidin.
DR Pfam; PF00666; Cathelicidin; 1.
DR ProDom; PD001838; Cathelicidin; 1.
DR PROSITE; PS00946; CATHLICIDINS_1; 1.
DR PROSITE; PS00947; CATHLICIDINS_2; 1.
DR SIGNAL.
FT SIGNAL 1 29 Potential.
FT CHAIN 30 156 Potential.
SQ SEQUENCE 156 AA; 17647 MW; BB8EA5D150288FFD CRC64;

Query Match 68.0%; Score 364; DB 2; Length 156;
Best Local Similarity 67.0%; Pred. No. 1.1e-30;
```

| | Matches | 67; | Conservative | 13; | Mismatches | 20; | Indels | 0; | Gaps | 0; |
|----|---------|---|---|-----|------------|-----|--------|----|------|----|
| Qy | 1 | QVLSYKAVLR | EATDGINQRSSDANLYRLDLDPRTMGDDPDTPKPVSVFTVKETVCBRTT | 60 | | | | | | |
| Db | 30 | QALSYSKAVLR | AVDGLNQRSDENLYRLLELDPLPKGDKSDTPKPVSMVMKETVCPRIM | 89 | | | | | | |
| Qy | 61 | QQSPEDCDFKKDGLVKRCMGTVTLLNQARGSFDIISCDKNK | 100 | | | | | | | |
| Db | 90 | KQTPEQCDFKENGVLVKCCVGTVILGPVKDHFDVSCGEPOR | 129 | | | | | | | |

RESULT 8

| | | | |
|------------|--|---------|---|
| PMFP23_PIG | STANDARD; | PRT; | 153 AA. |
| ID | PMFP23_PIG | | |
| AC | P49930; | | |
| DT | 01-OCT-1996 (Rel. 34, Created) | | |
| DT | 01-OCT-1996 (Rel. 34, Last sequence update) | | |
| DT | 13-SEP-2005 (Rel. 48, Last annotation update) | | |
| DB | Antibacterial peptide PMAP-23 precursor (Myeloid antibacterial peptide 23). | | |
| DB | Name=PMAP23; | | |
| OS | Sus scrofa (Pig). | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| OC | Mammalia; Euthera; Laurasiatheria; Cetartiodactyla; Suina; Suidae; | | |
| OC | Sus. | | |
| NCBI | TaxID=9823; | | |
| RP | [1] | | |
| RP | NUCLEOTIDE SEQUENCE, AND SYNTHESIS OF 131-153. | | |
| RC | TISSUE=Bone marrow; | | |
| RC | MEDLINE=84179144; PubMed=8132502; | | |
| RA | Zanetti M., Storici P., Tossi A., Scocchi M., Gennaro R.; | | |
| RT | "Molecular cloning and chemical synthesis of a novel antibacterial peptide derived from pig myeloid cells."; | | |
| RL | J. Biol. Chem. 269:7855-7858(1994). | | |
| CC | [2] | | |
| RP | NUCLEOTIDE SEQUENCE. | | |
| RC | TISSUE=Liver; | | |
| RC | Zhao C., Lehrer R.I.; | | |
| RL | Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases. | | |
| CC | -1- FUNCTION: Exerts antimicrobial activity against both Gram-positive and negative bacteria at concentrations of 2-16 micro molar. Its activity appears to be mediated by its ability to damage bacterial membranes. | | |
| CC | -1- SIMILARITY: Belongs to the cathelicidin family. | | |
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| CC | | | |
| CC | EMBL; L26053; AAA31103.1; -; mRNA. | | |
| DR | EMBL; Y16624; CAA76328.1; -; Genomic_DNA. | | |
| DR | PIR; A53421; A53421. | | |
| DR | HSP; P32196; ILXE. | | |
| DR | SMR; P49930; 30-130. | | |
| DR | InterPro; IPR01894; Cathelicidin. | | |
| DR | PANTHER; PTHR10206; Cathelicidin; 1. | | |
| DR | Pfam; PF00666; Cathelicidins; 1. | | |
| DR | ProDom; PD001838; Cathelicidin; 1. | | |
| DR | PROSITE; PS00946; CATHELICIDINS_1; 1. | | |
| DR | PROSITE; PS00947; CATHELICIDINS_2; 1. | | |
| DR | Antibiotic; Antimicrobial; Pyroglutamate carboxylic acid; Signal. | | |
| FT | SIGNAL | 1 | 29 Potential. |
| FT | PROPEP | 30 | 130 Potential. |
| FT | PEPTIDE | 131 | 153 Antibacterial peptide PMAP-23. |
| FT | MOD_RES | 30 | 30 Pyrrolidone carboxylic acid (By similarity). |
| FT | | | |
| FT | DISULFID | 85 | 96 By similarity. |
| FT | DISULFID | 107 | 124 By similarity. |
| FT | SEQUENCE | 153 AA; | 17486 MW; 7ADAA2286C206000 CRC64; |

Query Match 67.5%; Score 361; DB 1; Length 153;

Best Local Similarity 68.0%; Pred. No. 2.3e-30;
Matches 66; Conservative 17; Mismatches 14; Indels 0; Gaps 0;

QY 1 QVLSYKEAVLRALDGINQRSSDANLYRLLDLPRTWGDGPDTPKPVSVFTVKETVCPRTT 60
 :::|||||:-||:-||:-||:-||:-||:-||:-||:-||:-||:-||:-||:-||
Db 30 QALSYLEAVLRAVDRLNEQSSEANLYRLELDOPPKADEDPGTPKPVSVFTVKETVCPRT 89
 :::|||||:-||:-||:-||:-||:-||:-||:-||:-||:-||:-||:-||:-||

QY 61 QQSPEDCDFKKOGLVKRCMGTVTLNQARGSFDISCDK 97
 :::|||||:-||:-||:-||:-||:-||:-||:-||:-||:-||:-||:-||:-||
Db 90 RPPPELCDFKNGRVQCVCVTTLKEIRGNFDTICNQ 126
 :::|||||:-||:-||:-||:-||:-||:-||:-||:-||:-||:-||:-||:-||

RESULT 9

| BCTNS_CAPHI | STANDARD; | PRT; | 176 AA. |
|---|-----------|------|---------|
| ID BCTNS CAPHI | | | |
| AC P82018; | | | |
| DC 30-MAY-2000 (Rel. 39, Created) | | | |
| DT 30-MAY-2000 (Rel. 39, Last sequence update) | | | |
| DT 13-SEP-2005 (Rel. 48, Last annotation update) | | | |
| DE Bactenecin 5 precursor (Bac5) (ChBac5). | | | |
| GN Name=BAC5; | | | |
| OS Capra hircus (Goat). | | | |
| OC Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; | | | |
| OC Pecora; Bovidae; Caprinae; Capra. | | | |
| NCBI_TaxID=9925; | | | |
| [1] | | | |
| RN NUCLEOTIDE SEQUENCE OF 131-149 AND 151-153, AND PROTEIN SEQUENCE. | | | |
| RP TISSUE=Bone marrow, and Leukocyte; | | | |
| RC MEDLINE=99346202; PubMed=10417180; | | | |
| RX Shamova O., Brogden K.A., Zhao C., Nguyen T., Kokryakov V.N., | | | |
| RA Lehrer R.I.; | | | |
| RT "Purification and properties of proline-rich antimicrobial peptides | | | |
| RT from sheep and goat leukocytes."; | | | |
| RL Infect. Immun. 67:4106-4111(1999). | | | |
| CC -I- FUNCTION: Binds to the lipid A moiety of bacterial | | | |
| CC lipopolysaccharides (LPS), a glycolipid present in the outer | | | |
| CC membrane of all Gram-negative bacteria. Shows a potent | | | |
| CC antimicrobial activity against Gram-negative bacteria E.coli, | | | |
| CC S.typhimurium and P.aeruginosa. Less active against Gram-positive | | | |
| CC bacteria S.aureus, L.monocytogenes and B.subtilis. | | | |
| CC -I- DOMAIN: Bac5 sequence consists almost exclusively of X-P-P-Y | | | |
| CC repeats. | | | |
| CC -I- PTM: Elastase is responsible for its maturation. | | | |
| CC -I- SIMILARITY: Belongs to the cathelicidin family. | | | |
| CC ----- | | | |
| CC This Swiss-Prot entry is copyright. It is produced through a collaboration | | | |
| CC between the Swiss Institute of Bioinformatics and the EMBL Outstation - | | | |
| CC the European Bioinformatics Institute. There are no restrictions on its | | | |
| CC use as long as its content is in no way modified and this statement is not | | | |
| CC removed. | | | |
| CC ----- | | | |
| DR HSSP; P32196; 1KW1. | | | |
| DR SMR; P82018; 30-130. | | | |
| DR InterPro; IPR001894; Cathelicidin. | | | |
| DR PANTHER; PTHR10206; Cathelicidin; 1. | | | |
| DR Pfam; PF00666; Cathelcidins; 1. | | | |
| DR ProDom; PD001838; Cathelicidin; 1. | | | |
| DR PROSITE; PS00946; CATHELICIDINS_1; 1. | | | |
| DR POSITIVE; PS00947; CATHELICIDINS_2; 1. | | | |
| KW Amidation; Antibiotic; Antimicrobial; Direct protein sequencing; | | | |
| KW Pyrolidone carboxylic acid; Repeat; Signal. | | | |
| FT SIGNAL 1 29 Potential. | | | |
| FT FT PROPER 30 130 Bactenecin 5. | | | |
| FT PEPTIDE 131 173 Removed in mature form. | | | |
| FT PROPSP 174 176 Pyrolidone carboxylic acid (By | | | |
| FT MOD_RES 30 30 similarity). | | | |
| FT FT FT SIGNAL 1 29 Potential. | | | |
| FT MOD_RES 173 173 Proline amide (G-174 provides amide | | | |
| FT group). | | | |
| FT DISULFID 85 96 By similarity. | | | |
| FT DISULFID 107 124 By similarity. | | | |
| SQ SEQUENCE 176 AA; 19846 MW; 6FD7056C954E340A CRC64; | | | |

Query Match 67.5%; Score 361; DB 1; Length 176;
 Best Local Similarity 68.0%; Pred. No. 2.7e-30; Mismatches 14; Indels 0; Gaps 0;
 Matches 66; Conservative 17; Mismatches 14; Indels 0; Gaps 0;

QY 1 QVLSYKEAVLRADGINORSSDANLYRLDLDPRTMDGDDPTPKPVSTVKETVCPRTT 60
 DB 30 QALSRYEAVLRAGVQLNRSSEANLYRLLELDPAPNDEVDPTGTRKPVSTVKETVCPRTT 89
 QY 61 QQSPEDCDFKKGDLVKRCMGVTTLNQARGSFDISCDK 97
 DB 90 QQPPECDKFENGLVKQCVGTTLDPNSNDQFDINCNE 126

RESULT 10
 BCTN5_SHEEP
 ID BCTN5_SHEEP STANDARD; PRT; 176 AA.
 AC P79362; P79363;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Bactenecin 5 precursor (Bac5) (OaBac5).
 GN Name=BAC5;
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Caprinae; Ovis.
 OC NCBI_TaxID=9940;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA / MRNA].
 RC TISSUE=Liver;
 RX MEDLINE=9812117; PubMed=9461419; DOI=10.1016/S0378-1119(97)00569-6;
 RA Huttner K.M., Lambeth M.R., Burkin H.R., Broad T.E.;
 RT "Localization and genomic organization of sheep antimicrobial peptides
 gene";
 RL Gene 206:85-91(1998).
 CC -!- FUNCTION: Binds to the lipid A moiety of bacterial
 CC lipopolysaccharides (LPS), a glycolipid present in the outer
 CC membrane of all gram-negative bacteria. Potent antimicrobial
 CC activity (by similarity).
 CC -!- DOMAIN: BAC5 sequence consists almost exclusively of X-P-P-Y
 CC repeats.
 CC -!- PTM: Elastase is responsible for its maturation (By similarity).
 CC -!- SIMILARITY: Belongs to the cathelicidin family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; U60599; AAB49714.1; -; Genomic_DNA.
 DR EMBL; U60601; AAB49716.1; -; mRNA.
 DR HSSP; P32196; 1KWI.
 DR SMR; P79362; 30-130.
 DR InterPro; IPR001894; Cathelicidin.
 DR PANTHER; PTHR10206; Cathelicidin; 1.
 DR Pfam; PF00666; Cathelicidin; 1.
 DR ProDom; PD001838; Cathelicidin; 1.
 DR PROSITE; PS00946; CATHELICIDINS 1; 1.
 DR PROSITE; PS00947; CATHELICIDINS 2; 1.
 KW Amidation; Antibiotic; Antimicrobial; Pyrrolidone carboxylic acid;
 KW Repeat; Signal.
 FT SIGNAL 1 29 Potential.
 FT PROPEP 30 130 Bactenecin 5.
 FT PEPTIDE 131 173 Removed in mature form.
 FT PROPEP 174 176 Pyrrolidone carboxylic acid (By
 FT MOD_RES 30 30 similarity).
 FT MOD_RES 173 173 Proline amide (G-174 provides amide
 FT group).
 FT DISULFID 85 96 By similarity.
 FT DISULFID 107 124 By similarity.

FT CONFLICT 79 T -> R (in Ref. 1; AAB49716).
 SQ SEQUENCE 176 AA; 19842 MW; 05080026EA6FD5F7 CRC64;

Query Match 67.5%; Score 361; DB 1; Length 176;
 Best Local Similarity 68.0%; Pred. No. 2.7e-30; Mismatches 14; Indels 0; Gaps 0;
 Matches 66; Conservative 17; Mismatches 14; Indels 0; Gaps 0;

QY 1 QVLSYKEAVLRADGINORSSDANLYRLDLDPRTMDGDDPTPKPVSTVKETVCPRTT 60
 DB 30 QALSRYEAVLRAGVQLNRSSEANLYRLLELDPAPNDEVDPTGTRKPVSTVKETVCPRTT 89
 QY 61 QQSPEDCDFKKGDLVKRCMGVTTLNQARGSFDISCDK 97
 DB 90 QQPPECDKFENGLVKQCVGTTLDPNSNDQFDINCNE 126

RESULT 11
 Q4JFB9_CAPHI
 ID Q4JFB9_CAPHI PRELIMINARY; PRT; 176 AA.
 AC Q4JFB9;
 DT 13-SEP-2005 (TReMBLrel. 31, Created)
 DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
 DE Bac5 protein.
 GN Name=bac5;
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Caprinae; Capra.
 OC NCBI_TaxID=9925;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Bone marrow;
 RX MEDLINE=99346202; PubMed=10417180;
 RA Shanova O., Brogden K.A., Zhao C., Nguyen T., Kokryakov V.N.,
 RA Lehrer R.I.;
 RT "Purification and properties of proline-rich antimicrobial peptides
 RT from sheep and goat leukocytes";
 RL Infect. Immun. 67:4106-4111(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Bone marrow;
 RA Zhao C.;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Y18873; CAC80206.1; -; mRNA.
 SQ SEQUENCE 176 AA; 19846 MW; 6FD7056C954E340A CRC64;

Query Match 67.5%; Score 361; DB 2; Length 176;
 Best Local Similarity 68.0%; Pred. No. 2.7e-30; Mismatches 14; Indels 0; Gaps 0;
 Matches 66; Conservative 17; Mismatches 14; Indels 0; Gaps 0;

QY 1 QVLSYKEAVLRADGINORSSDANLYRLDLDPRTMDGDDPTPKPVSTVKETVCPRTT 60
 DB 30 QALSRYEAVLRAGVQLNRSSEANLYRLLELDPAPNDEVDPTGTRKPVSTVKETVCPRTT 89
 QY 61 QQSPEDCDFKKGDLVKRCMGVTTLNQARGSFDISCDK 97
 DB 90 QQPPECDKFENGLVKQCVGTTLDPNSNDQFDINCNE 126

RESULT 12
 BCTN1_BOVIN
 ID BCTN1_BOVIN STANDARD; PRT; 155 AA.
 AC P22226;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Cyclic dodecapeptide precursor (Bactenecin 1) (Bac1).
 GN Name=BAC1;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bos.

Db 30 QALSYREAVLRAVDQLNKSSEANLYRLLELDPPPKEDDENPNIPKPVSRVKTVCPRPT 89
QY 60 TQSPEDCDPKDGLVKRCMGVTTLNQARGSPDISC 95
Db 90 SQSPSEQCDPKENGLLKRCVGTTLQVGSNFDITC 125

RESULT 14
PR39 PIG
ID PR39 PIG STANDARD; PRT; 172 AA.
AC P80054; Q9TR84;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Antibacterial protein PR-39 precursor.
GN Name=PR39;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95350216; PubMed=7624374;
RA Gudmundsson G.H., Magnusson K.P., Chowdhary B.P., Johansson M.,
RA Andersson L., Boman H.G.;
RT "Structure of the gene for porcine peptide antibiotic PR-39, a
cathelin gene family member: comparative mapping of the locus for the
human peptide antibiotic FALL-39";
RL Proc. Natl. Acad. Sci. U.S.A. 92:7085-7089 (1995).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Bone marrow;
RX MEDLINE=94071853; PubMed=8250863;
RA Storici P., Zanetti M.;
RT "A cDNA derived from pig bone marrow cells predicts a sequence
identical to the intestinal antibacterial peptide PR-39";
RN Biochem. Biophys. Res. Commun. 196:1058-1065 (1993).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=96105365; PubMed=7498526; DOI=10.1016/0014-5793(95)01237-3;
RA Zhao C., Ganz T., Lehrer R.I.;
RT "Structures of genes for two cathelin-associated antimicrobial
peptides: prophenin-2 and PR-39";
RL FEBS Lett. 376:130-134 (1995).
RN [4]
RP PROTEIN SEQUENCE OF 131-169.
RC TISSUE=Intestine;
RX MEDLINE=92111534; PubMed=1765098;
RA Agerberth B., Lee J.-Y., Bergman T., Carlquist M., Boman H.G.,
RA Mutt V., Joernvall H.;
RT "Amino acid sequence of PR-39. Isolation from pig intestine of a new
member of the family of proline-arginine-rich antibacterial
peptides";
RL Eur. J. Biochem. 202:849-854 (1991).
RN [5]
RP PROTEIN SEQUENCE OF 131-164, AND FUNCTION.
RC TISSUE=Neutrophil;
RX MEDLINE=95088504; PubMed=7996056;
RA Shi J., Ross C.R., Chengappa M.M., Blecha F.;
RT "Identification of a proline-arginine-rich antibacterial peptide from
neutrophils that is analogous to PR-39, an antibacterial peptide from
the small intestine";
RL J. Leukoc. Biol. 56:807-811 (1994).
CC -!- FUNCTION: Exerts a potent antimicrobial activity against both
E.coli and B.megaterium.
CC -!- TISSUE SPECIFICITY: Small intestine and bone marrow.
CC -!- SIMILARITY: Belongs to the cathelicidin family.

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removed.

CC -----
CC EMBL; X87236; CAA60682.1; -; Genomic_DNA.
DR EMBL; L23825; AAA31109.1; -; mRNA.
DR EMBL; X89201; CAA61487.1; -; Genomic_DNA.
DR PIR; S68232; S68232.
DR HSSP; P32196; 1KWI.
DR SMR; P80054; 30-130.
DR InterPro; IPR001894; Cathelicidin.
DR PANTHER; PTHR10206; Cathelicidin; 1.
DR Pfam; PF00666; Cathelicidins; 1.
DR ProDom; PD001838; Cathelicidin; 1.
DR PROSITE; PS00946; CATHELICIDINS 1; 1.
DR PROSITE; PS00947; CATHELICIDINS 2; 1.
KW Amidation; Antibiotic; Antimicrobial; Direct protein sequencing;
KW Pyrrolidone carboxylic acid; Signal.
FT SIGNAL 1 29
FT PROPEP 30 130
FT CHAIN 131 169
FT MOD_RES 30 30
FT MOD_RES 169 169
FT DISULFID 85 96
FT DISULFID 107 124
FT CONFLICT 21 21
FT CONFLICT 29 29
FT CONFLICT 90 91
FT CONFLICT 117 119
FT CONFLICT 157 157
SQ SEQUENCE 172 AA; 19477 MW; 994B792798C0E133 CRC64;

Query Match 65.4%; Score 350; DB 1; Length 172;
Best Local Similarity 68.0%; Pred.No. 3.9e-29;
Matches 66; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 1 QVLSYKEAVLRAIDGINORSSDANLYRLLDPRPTMDGDPDTPKPVSTVKETVCPRPT 60
Db 30 QALSYREAVLRAVDRLNKSSEANLYRLLELDQPKADEDPCTPKPVSTVKETVCPRPT 89

QY 61 QQSPEDCDPKDGLVKRCMGVTTLNQARGSPDISCDK 97
Db 90 RQPELDCPKENGRVKQCVGTTLNPSIHSLDISCNE 126

RESULT 15
PF11 PIG
ID PF11 PIG STANDARD; PRT; 212 AA.
AC P51524;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Prophenin-1 precursor (PF-1) (C6) (Fragment).
OC Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Bone marrow;
RX MEDLINE=96042752; PubMed=7576250;
RA Strukelj B., Fungercar J., Kopitar G., Renko M., Lenarcic B.,
RA Berbic S., Turk V.;
RT "Molecular cloning and identification of a novel porcine cathelin-like
antibacterial peptide precursor";
RL Biol. Chem. Hoppe-Seyler 376:507-510 (1995).
RN [2]
RP PROTEIN SEQUENCE OF 131-209.
RC TISSUE=Blood;
RX MEDLINE=95212585; PubMed=7698355; DOI=10.1016/0014-5793(95)00210-2;
RA Harwig S.S.L., Kokryakov V.N., Swiderek K.M., Aleshina G.M., Zhao C.,

```

RA Lehrer R.I.;
RT "Prophenin-1, an exceptionally proline-rich antimicrobial peptide from
RL porcine leukocytes.";
RL FEBS Lett. 362:65-69(1995).
CC -I- FUNCTION: Exerts antimicrobial activity. It is more effective
CC against Gram-negative bacteria than Gram-positive bacteria.
CC -I- SIMILARITY: Belongs to the cathelicidin family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; X86031; CAA60023.1; -; mRNA.
CC F1R; S57330; S57330.
CC HSSP; P32196; 1LXE.
CC SMR; P51524; 14-110.
CC InterPro; IPR001894; Cathelicidin.
CC PANTHER; PTHR10206; Cathelicidin; 1.
CC Pfam; PF00666; Cathelicidins; 1.
CC ProDom; PD001838; Cathelicidins; 1.
CC PROSITE; PS00946; CATHELICIDINS_1; 1.
CC PROSITE; PS00947; CATHELICIDINS_2; 1.
CC Amidation; Antibiotic; Antimicrobial; Direct protein sequencing;
KW Pyrrolidone carboxylic acid; Repeat; Signal.
FT SIGNAL <1 13
FT PROPEP 14 130 Potential.
FT PEPTIDE 131 209 Prophenin-1.
FT PROPEP 210 212 Removed in mature form (Potential).
FT REPEAT 132 141 1.
FT REPEAT 142 151 2.
FT REPEAT 152 161 3.
FT REPEAT 162 171 4.
FT REPEAT 172 181 5.
FT REPEAT 182 191 6.
FT REPEAT 192 201 7.
FT REGION 132 201 7 X 10 AA tandem repeats.
FT COMBIAS 116 212 Pro-rich.
FT MOD_RES 14 14 Pyrrolidone carboxylic acid (By
FT MOD_RES 209 209 Proline amide (G-210 provides amide
FT DISULFID 69 80 group) (Potential).
FT DISULFID 91 108 By similarity.
FT NON_TER 1 1 By similarity.
SQ SEQUENCE 212 AA; 23956 MW; A315414C90DBF423 CRC64;

Query Match 65.4%; Score 350; DB 1; Length 212;
Best Local Similarity 64.4%; Pred. No. 5e-29;
Matches 65; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

QY 1 QVLSYKEAVLRATDGINORSSDANLYRLDLDPRPTMDGDDPTPKVSPVTVKTVCPRTT 60
Db |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
14 QALSYKEAVLRVDRLNQSSSEANLYRLLELQPPKADEDFGTPKPVSPVTVKTVCPRT 73
QY 61 QQSPEDCDFKKGGLVKRCMGTVTLNQARGSFDISCDKNKR 101
Db |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
74 RQPELCDFKENGVRKQCVTVTLQDKPLDITCNQGVRR 114

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Search completed: January 12, 2006, 21:50:32
 Job time : 49.1956 secs

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| Result No. | Score | Query | | Length | DB | ID | Description |
|------------|-------|-------|-----|--------|---------------------|----|----------------------|
| | | Match | \$ | | | | |
| 1 | 535 | 100.0 | 152 | 2 | US-09-513-999C-7862 | | Sequence 7862, Appli |
| 2 | 535 | 100.0 | 170 | 1 | US-08-313-681A-2 | | Sequence 2, Appli |
| 3 | 535 | 100.0 | 170 | 2 | US-09-322-911-2 | | Sequence 2, Appli |
| 4 | 535 | 100.0 | 170 | 2 | US-09-317-340-32 | | Sequence 32, Appli |
| 5 | 367 | 68.6 | 170 | 2 | US-09-917-340-33 | | Sequence 33, Appli |
| 6 | 364 | 68.0 | 156 | 2 | US-09-917-340-35 | | Sequence 35, Appli |
| 7 | 354 | 66.2 | 155 | 2 | US-09-917-340-29 | | Sequence 29, Appli |
| 8 | 352.5 | 65.9 | 159 | 2 | US-09-917-340-34 | | Sequence 34, Appli |
| 9 | 347 | 64.9 | 147 | 1 | US-08-243-879A-38 | | Sequence 38, Appli |
| 10 | 347 | 64.9 | 147 | 1 | US-08-499-523-4 | | Sequence 4, Appli |
| 11 | 347 | 64.9 | 147 | 2 | US-09-128-345-4 | | Sequence 4, Appli |
| 12 | 347 | 64.9 | 147 | 2 | US-09-385-328-4 | | Sequence 4, Appli |
| 13 | 347 | 64.9 | 149 | 1 | US-08-243-879A-36 | | Sequence 36, Appli |
| 14 | 347 | 64.9 | 149 | 1 | US-08-243-879A-40 | | Sequence 40, Appli |
| 15 | 347 | 64.9 | 149 | 1 | US-08-243-879A-42 | | Sequence 42, Appli |
| 16 | 347 | 64.9 | 149 | 1 | US-08-499-523-2 | | Sequence 2, Appli |
| 17 | 347 | 64.9 | 149 | 1 | US-08-499-523-6 | | Sequence 6, Appli |
| 18 | 347 | 64.9 | 149 | 1 | US-08-499-523-8 | | Sequence 8, Appli |
| 19 | 347 | 64.9 | 149 | 1 | US-08-499-523-10 | | Sequence 10, Appli |
| 20 | 347 | 64.9 | 149 | 2 | US-09-128-345-2 | | Sequence 2, Appli |
| 21 | 347 | 64.9 | 149 | 2 | US-09-128-345-6 | | Sequence 6, Appli |
| 22 | 347 | 64.9 | 149 | 2 | US-09-128-345-8 | | Sequence 8, Appli |
| 23 | 347 | 64.9 | 149 | 2 | US-09-128-345-10 | | Sequence 10, Appli |
| 24 | 347 | 64.9 | 149 | 2 | US-09-385-328-2 | | Sequence 2, Appli |
| 25 | 347 | 64.9 | 149 | 2 | US-09-385-328-6 | | Sequence 6, Appli |
| 26 | 347 | 64.9 | 149 | 2 | US-09-385-328-8 | | Sequence 8, Appli |
| 27 | 343 | 64.1 | 171 | 1 | US-08-313-681A-4 | | Sequence 4, Appli |

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;
; TITLE OF INVENTION: Lipopolyeaccharide Binding and Anti-Coagulant Activity
;
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,681A
;
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Heelin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15325-9-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-08-313-681A-2
;
; Query Match 100.0%; Score 535; DB 1; Length 170;
; Best Local Similarity 100.0%; Pred. No. 8.2e-60;
; Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY 1 QVLSYKEAVLRADIGINQRSSDANLYRLDLLDPRPTMDGDDTPKPVSTTKETVCPRTT 60
; |
; DB 31 QVLSYKEAVLRADIGINQRSSDANLYRLDLLDPRPTMDGDDTPKPVSTTKETVCPRTT 90
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;
; QY 61 QQSPEDCDFKKGGLVKRCMGVTTLNQARGSFDISCDKDKNR 101
; |
; DB 91 QQSPEDCDFKKGGLVKRCMGVTTLNQARGSFDISCDKDKNR 131
; |
;
; RESULT 3
; US-09-322-911-2
; Sequence 2, Application US/09322911
; Patent No. 6103888
; GENERAL INFORMATION:
; APPLICANT: Larrick, James W.
; APPLICANT: Wright, Susan C.
; APPLICANT: Hirata, Mishinasa
; APPLICANT: Balint, Robert F.
; TITLE OF INVENTION: Human Cationic Proteins Having
; TITLE OF INVENTION: Lipopolyeaccharide Binding and Anti-Coagulant Activity
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/322,911
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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/691,280
; FILING DATE: August 1, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/916,761
; FILING DATE: July 17, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/916,765
; FILING DATE: July 17, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06731
; FILING DATE: July 15, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/313,681
; FILING DATE: September 27, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 15325-000920
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-09-322-911-2
;
; Query Match 100.0%; Score 535; DB 2; Length 170;
; Best Local Similarity 100.0%; Pred. No. 8.2e-60;
; Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 QVLSYKEAVLRADIGINQRSSDANLYRLDLLDPRPTMDGDDTPKPVSTTKETVCPRTT 60
; |
; DB 31 QVLSYKEAVLRADIGINQRSSDANLYRLDLLDPRPTMDGDDTPKPVSTTKETVCPRTT 90
; |
;
; QY 61 QQSPEDCDFKKGGLVKRCMGVTTLNQARGSFDISCDKDKNR 101
; |
; DB 91 QQSPEDCDFKKGGLVKRCMGVTTLNQARGSFDISCDKDKNR 131
; |
;
; RESULT 4
; US-09-917-340-32
; Sequence 32, Application US/09917340
; Patent No. 6696238
; GENERAL INFORMATION:
; APPLICANT: Murphy, Christopher J.
; APPLICANT: McNulty, Jonathan F.
; APPLICANT: Reid, Ted W.
; TITLE OF INVENTION: Transplant Media
; FILE REFERENCE: TPLANT-06468
; CURRENT APPLICATION NUMBER: US/09/917,340
; CURRENT FILING DATE: 2001-07-29
; PRIOR APPLICATION NUMBER: 60/221,632
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/290,932
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
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; US-09-917-340-32
;
; Query Match 100.0%; Score 535; DB 2; Length 170;
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Best Local Similarity 100.0%; Pred. No. 8.2e-60;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVLSYKEAVLRAIDGINQRSSDANLYRLDLLDPRPTWDGDPDTPKPVSFYTKETVCPRTT 60
Db 31 QVLSYKEAVLRAIDGINQRSSDANLYRLDLLDPRPTWDGDPDTPKPVSFYTKETVCPRTT 90

Qy 61 QQSPEDCDFKKGGLVKRCMGTVTILNQARGSFDISCDKNR 101
Db 91 QQSPEDCDFKKGGLVKRCMGTVTILNQARGSFDISCDKNR 131

RESULT 5
US-09-917-340-33
; Sequence 33, Application US/09917340
; Patent No. 6696238
; GENERAL INFORMATION:
; APPLICANT: Murphy, Christopher J.
; APPLICANT: McNulty, Jonathan F.
; TITLE OF INVENTION: Transplant Media
; FILE REFERENCE: TPLANT-06468
; CURRENT APPLICATION NUMBER: US/09/917,340
; CURRENT FILING DATE: 2001-07-29
; PRIOR APPLICATION NUMBER: 60/221,632
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/290,932
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Equus caballus
US-09-917-340-33

Query Match 68.6%; Score 367; DB 2; Length 170;
Best Local Similarity 68.0%; Pred. No. 1.7e-38;
Matches 68; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

Qy 1 QVLSYKEAVLRAIDGINQRSSDANLYRLDLLDPRPTWDGDPDTPKPVSFYTKETVCPRTT 60
Db 30 QVLSYKEAVLRAIDGINQRSSDANLYRLDLLDPRPTWDGDPDTPKPVSFYTKETVCPRIM 89

Qy 61 QQSPEDCDFKKGGLVKRCMGTVTILNQARGSFDISCDKNK 100
Db 90 KQTPEQCDKFENGLVKQCVGTIVLDPVKDYFDASCDSPQR 129

RESULT 6
US-09-917-340-35
; Sequence 35, Application US/09917340
; Patent No. 6696238
; GENERAL INFORMATION:
; APPLICANT: Murphy, Christopher J.
; APPLICANT: McNulty, Jonathan F.
; TITLE OF INVENTION: Transplant Media
; FILE REFERENCE: TPLANT-06468
; CURRENT APPLICATION NUMBER: US/09/917,340
; CURRENT FILING DATE: 2001-07-29
; PRIOR APPLICATION NUMBER: 60/221,632
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/290,932
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 156
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; TYPE: PRT
; ORGANISM: Equus asinus
US-09-917-340-35

Query Match 68.0%; Score 364; DB 2; Length 156;
Best Local Similarity 67.0%; Pred. No. 3.6e-38;
Matches 67; Conservative 13; Mismatches 20; Indels 0; Gaps 0;

Qy 1 QVLSYKEAVLRAIDGINQRSSDANLYRLDLLDPRPTWDGDPDTPKPVSFYTKETVCPRTT 60
Db 30 QVLSYKEAVLRAIDGINQRSSDANLYRLDLLDPRPTWDGDPDTPKPVSFYTKETVCPRIM 89

Qy 61 QQSPEDCDFKKGGLVKRCMGTVTILNQARGSFDISCDKNK 100
Db 90 KQTPEQCDKFENGLVKQCVGTIVLDPVKDYFDASCDSPQR 129

RESULT 7
US-09-917-340-29
; Sequence 29, Application US/09917340
; Patent No. 6696238
; GENERAL INFORMATION:
; APPLICANT: Murphy, Christopher J.
; APPLICANT: McNulty, Jonathan F.
; TITLE OF INVENTION: Transplant Media
; FILE REFERENCE: TPLANT-06468
; CURRENT APPLICATION NUMBER: US/09/917,340
; CURRENT FILING DATE: 2001-07-29
; PRIOR APPLICATION NUMBER: 60/221,632
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/290,932
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-917-340-29

Query Match 66.2%; Score 354; DB 2; Length 155;
Best Local Similarity 67.7%; Pred. No. 6.6e-37;
Matches 65; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

Qy 1 QVLSYKEAVLRAIDGINQRSSDANLYRLDLLDPRPTWDGDPDTPKPVSFYTKETVCPRTT 60
Db 30 QVLSYKEAVLRAIDGINQRSSDANLYRLDLLDPRPTWDGDPDTPKPVSFYTKETVCPRIM 89

Qy 61 QQSPEDCDFKKGGLVKRCMGTVTILNQARGSFDISCD 96
Db 90 QQPPEQCDKFENGLLKKCEGTIVLDQVRGNFDITCN 125

RESULT 8
US-09-917-340-34
; Sequence 34, Application US/09917340
; Patent No. 6696238
; GENERAL INFORMATION:
; APPLICANT: Murphy, Christopher J.
; APPLICANT: McNulty, Jonathan F.
; TITLE OF INVENTION: Transplant Media
; FILE REFERENCE: TPLANT-06468
; CURRENT APPLICATION NUMBER: US/09/917,340
; CURRENT FILING DATE: 2001-07-29
; PRIOR APPLICATION NUMBER: 60/221,632
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 156
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RESULT 10
US-08-499-523-4
; Sequence 4, Application US/08499523
; Patent No. 5804558
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S. L.
; APPLICANT: KOKRYAKOV, VLADIMIR N.
; TITLE OF INVENTION: PROTEGRINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/499,523
; FILING DATE: 07-JUL-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2000-0540.24
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 147 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-499-523-4

Query Match 64.9%; Score 347; DB 1; Length 147;
Best Local Similarity 66.0%; Pred. No. 4.7e-36;
Matches 64; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

Qy 1 QVLSYKEAVLNRADTGINORSSDANLYRLDLDPRPTWGDGDDPKPVSFTVKETVCPRTT 60
Db 30 QALSUREAVLNRVDRNLNQSSEANLYRLLEDQPPKADEPGTTPKPSFTVKETVCPRPT 89
Qy 61 QSQPEPCDFKKGGLVKRCMGTVTLNQAGSFDISCDK 97
Db 90 RQPELPCDFKENGVRKQCVGTVLQDKPLDITCNE 126

RESULT 11
US-09-128-345-4
; Sequence 4, Application US/09128345
; Patent No. 615936
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S. L.
; APPLICANT: KOKRYAKOV, VLADIMIR N.
; TITLE OF INVENTION: PROTEGRINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA

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OM protein - protein search, using sw model

Run on: January 12, 2006, 21:45:40 ; Search time 41.7417 Seconds
(without alignments)
1010.998 Million cell updates/sec

Title: US-10-815-562-2_COPY_31_131
Perfect score: 535
Sequence: 1 QVLSYKEAVLRADGINQRS.....VTLNQARGSFDISCDKNKR 101

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main.*
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2: /cgm2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgm2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgm2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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6: /cgm2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 535 | 100.0 | 170 | 3 | US-09-917-340-32 |
| 2 | 535 | 100.0 | 170 | 4 | US-10-603-566-51 |
| 3 | 535 | 100.0 | 170 | 4 | US-10-344-709C-11 |
| 4 | 535 | 100.0 | 170 | 5 | US-10-844-837-32 |
| 5 | 535 | 100.0 | 170 | 5 | US-10-777-683-4 |
| 6 | 535 | 100.0 | 170 | 5 | US-10-909-119-47 |
| 7 | 535 | 100.0 | 170 | 5 | US-10-657-851-32 |
| 8 | 535 | 100.0 | 170 | 5 | US-10-893-485-51 |
| 9 | 535 | 100.0 | 170 | 5 | US-10-287-436A-513 |
| 10 | 535 | 100.0 | 170 | 5 | US-10-287-436A-1204 |
| 11 | 367 | 68.6 | 170 | 3 | US-09-917-340-33 |
| 12 | 367 | 68.6 | 170 | 5 | US-10-844-837-33 |
| 13 | 367 | 68.6 | 170 | 5 | US-10-909-119-48 |
| 14 | 367 | 68.6 | 170 | 5 | US-10-657-851-33 |
| 15 | 364 | 68.0 | 156 | 3 | US-09-917-340-35 |
| 16 | 364 | 68.0 | 156 | 5 | US-10-844-837-35 |
| 17 | 364 | 68.0 | 156 | 5 | US-10-909-119-50 |
| 18 | 364 | 68.0 | 156 | 5 | US-10-657-851-35 |
| 19 | 354 | 66.2 | 155 | 3 | US-09-917-340-29 |
| 20 | 354 | 66.2 | 155 | 4 | US-10-344-709C-8 |
| 21 | 354 | 66.2 | 155 | 5 | US-10-844-837-29 |
| 22 | 354 | 66.2 | 155 | 5 | US-10-909-119-44 |
| 23 | 354 | 66.2 | 155 | 5 | US-10-657-851-29 |
| 24 | 352.5 | 65.9 | 159 | 3 | US-09-917-340-34 |
| 25 | 352.5 | 65.9 | 159 | 5 | US-10-844-837-34 |
| 26 | 352.5 | 65.9 | 159 | 5 | US-10-909-119-49 |
| 27 | 352.5 | 65.9 | 159 | 5 | US-10-657-851-34 |

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28      347      64.9      147      3      US-09-539-443-4      Sequence 4, Appli
29      347      64.9      147      4      US-10-627-829-4      Sequence 4, Appli
30      347      64.9      149      3      US-09-539-443-2      Sequence 2, Appli
31      347      64.9      149      3      US-09-539-443-6      Sequence 6, Appli
32      347      64.9      149      3      US-09-539-443-8      Sequence 8, Appli
33      347      64.9      149      3      US-09-539-443-10     Sequence 10, Appli
34      347      64.9      149      4      US-10-627-829-2      Sequence 2, Appli
35      347      64.9      149      4      US-10-627-829-6      Sequence 6, Appli
36      347      64.9      149      4      US-10-627-829-8      Sequence 8, Appli
37      347      64.9      149      4      US-10-627-829-10     Sequence 10, Appli
38      343      64.1      171      4      US-10-344-709C-7      Sequence 7, Appli
39      340.5      63.6      160      3      US-09-917-340-36      Sequence 36, Appli
40      340.5      63.6      160      5      US-10-844-837-36      Sequence 36, Appli
41      340.5      63.6      160      5      US-10-909-119-51      Sequence 51, Appli
42      340.5      63.6      160      5      US-10-657-851-36      Sequence 51, Appli
43      340      63.6      176      3      US-09-917-340-28      Sequence 28, Appli
44      340      63.6      176      4      US-10-344-709C-9      Sequence 9, Appli
45      340      63.6      176      5      US-10-844-837-28      Sequence 28, Appli

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ALIGNMENTS

RESULT 1

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US-09-917-340-32
; Sequence 32, Application US/09917340
; Patent No. US20020090369A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Christopher J.
; APPLICANT: Meanulty, Jonathan P.
; APPLICANT: Reid, Ted W.
; TITLE OF INVENTION: Transplant Media
; FILE REFERENCE: TPLANT-06468
; CURRENT APPLICATION NUMBER: US/09/917,340
; CURRENT FILING DATE: 2001-07-29
; PRIOR APPLICATION NUMBER: 60/221,632
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/290,932
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-917-340-32

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Query Match      100.0%; Score 535; DB 3; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-52;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 QVLSYKEAVLRADGINQRS DANLYRLDLLDPRPTWDGDDPTPKPVSTVTKETVCPRTT 60
Db      31 QVLSYKEAVLRADGINQRS DANLYRLDLLDPRPTWDGDDPTPKPVSTVTKETVCPRTT 90
Qy      61 QQSPEDCDFKXGLVKRCMGVTTLNQARGSFDISCDKNKR 101
Db      91 QQSPEDCDFKXGLVKRCMGVTTLNQARGSFDISCDKNKR 131

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RESULT 2

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US-10-603-566-51
; Sequence 51, Application US/10603566
; Publication No. US20040086966A1
; GENERAL INFORMATION:
; APPLICANT: Wittamer, Valerie
; APPLICANT: Communi, David
; APPLICANT: Vandenbogaerde, Ann
; APPLICANT: Detheux, Michel
; APPLICANT: Parmentier, Marc
; TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of ChemerinR

```

```
; FILE REFERENCE: 9409/2212
; CURRENT APPLICATION NUMBER: US/10/603,566
; CURRENT FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US 60/303,858
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 09/905,253
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 10/201,187
; PRIOR FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-603-566-51

Query Match      100.0%; Score 535; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-52;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRTMDGDDTPKPVSVFTVKETVCPRTT 60
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Db  31 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRTMDGDDTPKPVSVFTVKETVCPRTT 90
    |||||

Qy  61 QQSPEDCDFKKGGLVKRCMGTVTLNQARGSPDISCDKDKNR 101
    |||||
Db  91 QQSPEDCDFKKGGLVKRCMGTVTLNQARGSPDISCDKDKNR 131
    |||||

RESULT 3
US-10-344-709C-11
; Sequence 11, Application US/10344709C
; Publication No. US20040170642A1
; GENERAL INFORMATION:
; APPLICANT: JORG FRITZ ET AL.
; TITLE OF INVENTION: Vaccine which comprises at least one antigen and a cathelicidin
; FILE REFERENCE: derived antimicrobial peptide or a derivative thereof
; FILE REFERENCE: SONN.030US
; CURRENT APPLICATION NUMBER: US/10/344,709C
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: PCT/EP01/09529
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: A 1416/2000
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 11
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
; US-10-344-709C-11

Query Match      100.0%; Score 535; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-52;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRTMDGDDTPKPVSVFTVKETVCPRTT 60
    |||||
Db  31 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRTMDGDDTPKPVSVFTVKETVCPRTT 90
    |||||

Qy  61 QQSPEDCDFKKGGLVKRCMGTVTLNQARGSPDISCDKDKNR 101
    |||||
Db  91 QQSPEDCDFKKGGLVKRCMGTVTLNQARGSPDISCDKDKNR 131
    |||||

RESULT 4
US-10-844-837-32
; Sequence 32, Application US/10844837
; Publication No. US20050014932A1
; GENERAL INFORMATION:
; APPLICANT: Centanni, John M.
; TITLE OF INVENTION: Human Skin Equivalents Expressing Exogenous Polypeptides
; FILE REFERENCE: STRATA-09123
; CURRENT APPLICATION NUMBER: US/10/909,119
```

```
; APPLICANT: Imboden, Michael
; APPLICANT: Homan, Jane
; APPLICANT: Bremel, Robert D.
; TITLE OF INVENTION: Targeted Biocides
; FILE REFERENCE: IOGEN-09014
; CURRENT APPLICATION NUMBER: US/10/844,837
; CURRENT FILING DATE: 2004-05-13
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-844-837-32

Query Match      100.0%; Score 535; DB 5; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-52;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRTMDGDDTPKPVSVFTVKETVCPRTT 60
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Db  31 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRTMDGDDTPKPVSVFTVKETVCPRTT 90
    |||||

Qy  61 QQSPEDCDFKKGGLVKRCMGTVTLNQARGSPDISCDKDKNR 101
    |||||
Db  91 QQSPEDCDFKKGGLVKRCMGTVTLNQARGSPDISCDKDKNR 131
    |||||

RESULT 5
US-10-777-683-4
; Sequence 4, Application US/10777683
; Publication No. US20050032117A1
; GENERAL INFORMATION:
; APPLICANT: Richard B. Moss
; APPLICANT: Akitoshi Ishizaka
; APPLICANT: Teruo Kiriakae
; TITLE OF INVENTION: Method for Assessment of Cystic Lung Fibrosis
; FILE REFERENCE: Q74236
; CURRENT APPLICATION NUMBER: US/10/777,683
; CURRENT FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: US 60/447,310
; PRIOR FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-777-683-4

Query Match      100.0%; Score 535; DB 5; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-52;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRTMDGDDTPKPVSVFTVKETVCPRTT 60
    |||||
Db  31 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRTMDGDDTPKPVSVFTVKETVCPRTT 90
    |||||

Qy  61 QQSPEDCDFKKGGLVKRCMGTVTLNQARGSPDISCDKDKNR 101
    |||||
Db  91 QQSPEDCDFKKGGLVKRCMGTVTLNQARGSPDISCDKDKNR 131
    |||||

RESULT 6
US-10-909-119-47
; Sequence 47, Application US/10909119
; Publication No. US20050079578A1
; GENERAL INFORMATION:
; APPLICANT: Centanni, John M.
; TITLE OF INVENTION: Human Skin Equivalents Expressing Exogenous Polypeptides
; FILE REFERENCE: STRATA-09123
; CURRENT APPLICATION NUMBER: US/10/909,119
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; CURRENT FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 47
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-909-119-47

Query Match      100.0%; Score 535; DB 5; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-52;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVLSYKEAVLRADIGINQRSSDANLYRLDLDPRPTMDGDDPTPKPVSTVKTVCPRRTT 60
Db 31 QVLSYKEAVLRADIGINQRSSDANLYRLDLDPRPTMDGDDPTPKPVSTVKTVCPRRTT 90

Qy 61 QQSPEDCDPCKDGLVKRCMGTVTLNQARGSPDISCDKDKNR 101
Db 91 QQSPEDCDPCKDGLVKRCMGTVTLNQARGSPDISCDKDKNR 131

RESULT 7
US-10-657-851-32
; Sequence 32, Application US/10657851
; Publication No. US20050089836A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Christopher J.
; APPLICANT: McNulty, Jonathan F.
; APPLICANT: Reid, Ted W.
; TITLE OF INVENTION: Transplant Media
; FILE REFERENCE: TPLANT-06468
; CURRENT APPLICATION NUMBER: US/10/657,851
; CURRENT FILING DATE: 2003-09-09
; PRIOR FILING DATE: US/09/917,340
; PRIOR APPLICATION NUMBER: 60/221,632
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/290,932
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 32
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-657-851-32

Query Match      100.0%; Score 535; DB 5; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-52;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVLSYKEAVLRADIGINQRSSDANLYRLDLDPRPTMDGDDPTPKPVSTVKTVCPRRTT 60
Db 31 QVLSYKEAVLRADIGINQRSSDANLYRLDLDPRPTMDGDDPTPKPVSTVKTVCPRRTT 90

Qy 61 QQSPEDCDPCKDGLVKRCMGTVTLNQARGSPDISCDKDKNR 101
Db 91 QQSPEDCDPCKDGLVKRCMGTVTLNQARGSPDISCDKDKNR 131

RESULT 8
US-10-893-485-51
; Sequence 51, Application US/10893485
; Publication No. US20050155090A1
; GENERAL INFORMATION:
; APPLICANT: Wittamer, Valerie
; APPLICANT: Communi, David
; APPLICANT: Vandenbogaerde, Ann
; APPLICANT: Detheux, Michel
; APPLICANT: Parmentier, Marc

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; TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of ChemerinR
; FILE REFERENCE: 9409/2045C
; CURRENT APPLICATION NUMBER: US/10/893,485
; CURRENT FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: US 60/303,858
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US10/603,566
; PRIOR FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US 09/905,253
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 10/201,187
; PRIOR FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 51
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-893-485-51

Query Match      100.0%; Score 535; DB 5; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-52;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVLSYKEAVLRADIGINQRSSDANLYRLDLDPRPTMDGDDPTPKPVSTVKTVCPRRTT 60
Db 31 QVLSYKEAVLRADIGINQRSSDANLYRLDLDPRPTMDGDDPTPKPVSTVKTVCPRRTT 90

Qy 61 QQSPEDCDPCKDGLVKRCMGTVTLNQARGSPDISCDKDKNR 101
Db 91 QQSPEDCDPCKDGLVKRCMGTVTLNQARGSPDISCDKDKNR 131

RESULT 9
US-10-287-436A-513
; Sequence 513, Application US/10287436A
; Publication No. US20050202421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 513
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-436A-513

Query Match      100.0%; Score 535; DB 5; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-52;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVLSYKEAVLRADIGINQRSSDANLYRLDLDPRPTMDGDDPTPKPVSTVKTVCPRRTT 60
Db 31 QVLSYKEAVLRADIGINQRSSDANLYRLDLDPRPTMDGDDPTPKPVSTVKTVCPRRTT 90

Qy 61 QQSPEDCDPCKDGLVKRCMGTVTLNQARGSPDISCDKDKNR 101
Db 91 QQSPEDCDPCKDGLVKRCMGTVTLNQARGSPDISCDKDKNR 131

RESULT 10
US-10-287-436A-1204
; Sequence 1204, Application US/10287436A
; Publication No. US20050202421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER

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Search completed: January 12, 2006, 21:54:02
Job time : 41.7417 secs

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Db 141 DGNLYLLDMG-----SGTIK-----VKATQKANDGEWYHVDIQDGR-- 179
Qy 77 RCMGTVTLNQARGSFDISCDK 98
Db 180 --SGTISVNSRRTPTFTASGESE 199

RESULT 2
US-11-000-463-348
; Sequence 348, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; PRIOR FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 348
; LENGTH: 1091
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-348

Query Match 11.4%; Score 61; DB 7; Length 1091;
Best Local Similarity 25.8%; Pred. No. 21;
Matches 22; Conservative 11; Mismatches 21; Indels 28; Gaps 4;

Qy 22 DANLYRLDLLDPRMTDGDPTPKVPSFTVKETVCPRTTQSPED-----COFKKGLVK 76
Db 141 DGNLYLLDMG-----SGTIK-----VKATQKANDGEWYHVDIQDGR-- 179
Qy 77 RCMGTVTLNQARGSFDISCDK 98
Db 180 --SGTISVNSRRTPTFTASGESE 199

RESULT 3
US-11-147-047-47
; Sequence 47, Application US/11147047
; Publication No. US2005026068A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdock, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall P.
; APPLICANT: Xiang, Zhaoying
; TITLE OF INVENTION: NOVEL COMPOUNDS
```

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; FILE REFERENCE: GP50016
; CURRENT APPLICATION NUMBER: US/11/147,047
; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US/10/221,097
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: PCT/US01/07143
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/187,107
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/236,874
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/188,916
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/237,846
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 47
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-147-047-47

Query Match 11.2%; Score 60; DB 7; Length 349;
Best Local Similarity 28.4%; Pred. No. 6.5;
Matches 19; Conservative 6; Mismatches 30; Indels 12; Gaps 2;

Qy 22 DANLYRLDLLDPRMTDGDPTPKVPSFTVKETVCPRTTQSPEDCDCKDGLVKR 77
Db 234 DENSSAGLDIPGPPCTKASPEPAKPKFGABPEPSTACPKQKRRFAS-----VRR 285
Qy 78 CMGTVTLL 84
Db 286 AMGTVII 292

RESULT 4
US-10-467-657-3750
; Sequence 3750, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3750
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3750

Query Match 11.1%; Score 59.5; DB 6; Length 389;
Best Local Similarity 26.8%; Pred. No. 8.6;
Matches 22; Conservative 10; Mismatches 31; Indels 19; Gaps 3;

Qy 6 KEAVLRAIDGINQRSSDANLYRLI-----DLDPRTWDGDDPTPKVPSFTVKETVCPRTT 60
Db 302 KEAAQTAVELVRRKPDNLNGVRLIGLKLSDLPKADAD-----MMRSVIGRQL 351
Qy 61 QQSP-----EDCDPKKGLVKRC 78
Db 352 QRSVMYCRNCHFAKSVQFFWHC 373
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RESULT 5
US-11-055-822-68
; Sequence 68, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Krogner, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; METABOLIC PATHWAY PROTEINS
; FILE REFERENCE: BGI-121CPN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR FILING DATE: 09/606,740
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 68
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-68

Query Match 11.1%; Score 59.5; DB 7; Length 468;
Best Local Similarity 32.1%; Pred. No. 11;
Matches 18; Conservative 9; Mismatches 20; Indels 9; Gaps 2;

Qy 3 LSYKEAVLRADGINQR-----SSDANLYRLDLLDPRPTMGD-----PDTKPVSP 49
Db 315 LTLSSAVARSLSGMLRMVQLALSSVERIFVIDLQPERTDPAHPLSLPDTPLGLSP 370

RESULT 6
US-10-667-295-43
; Sequence 43, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Mascia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(102)

US-10-667-295-43
; OTHER INFORMATION: Ceres Seq. ID no. 6425770
US-10-667-295-43
Query Match 10.8%; Score 58; DB 6; Length 141;
Best Local Similarity 23.3%; Pred. No. 3.6;
Matches 20; Conservative 10; Mismatches 24; Indels 32; Gaps 2;

Qy 8 AVLRAIDGINQRSSDANLYRLDLLDPRPTMGDPTPKPVSFYKVTVCPRTTQOSPDC 67
Db 74 SVVGAVDGV-----AMEVDVDSAK-----TNSNSDK 101

Qy 68 DPKKGLVKRCMGTVTLNQARGSPDI 93
Db 102 SEKDGRKRLCVGSQALNYRDRHMEI 127

RESULT 7
US-10-667-295-42
; Sequence 42, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Mascia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(141)
; OTHER INFORMATION: Ceres Seq. ID no. 6425769
US-10-667-295-42

Query Match 10.8%; Score 58; DB 6; Length 141;
Best Local Similarity 23.3%; Pred. No. 3.6;
Matches 20; Conservative 10; Mismatches 24; Indels 32; Gaps 2;

Qy 8 AVLRAIDGINQRSSDANLYRLDLLDPRPTMGDPTPKPVSFYKVTVCPRTTQOSPDC 67
Db 74 SVVGAVDGV-----AMEVDVDSAK-----TNSNSDK 101

Qy 68 DPKKGLVKRCMGTVTLNQARGSPDI 93
Db 102 SEKDGRKRLCVGSQALNYRDRHMEI 127

RESULT 8
US-11-100-183-15
; Sequence 15, Application US/11100183
; Publication No. US2005027074A1
; GENERAL INFORMATION:
; APPLICANT: Stratagene California
; TITLE OF INVENTION: Compositions And Methods For Reverse Transcription
; FILE REFERENCE: 25436/2452
; CURRENT APPLICATION NUMBER: US/11/100,183
; CURRENT FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: US 60/559,810
; PRIOR FILING DATE: 2004-04-06
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 15
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Pasteurella multocida
US-11-100-183-15
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; OTHER INFORMATION: Ceres Seq. ID no. 6425770
US-10-667-295-43
Query Match 10.8%; Score 58; DB 6; Length 102;
Best Local Similarity 23.3%; Pred. No. 2.4;
Matches 20; Conservative 10; Mismatches 24; Indels 32; Gaps 2;

Qy 8 AVLRAIDGINQRSSDANLYRLDLLDPRPTMGDPTPKPVSFYKVTVCPRTTQOSPDC 67
Db 35 SVVGAVDGV-----AMEVDVDSAK-----TNSNSDK 62

Qy 68 DPKKGLVKRCMGTVTLNQARGSPDI 93
Db 63 SEKDGRKRLCVGSQALNYRDRHMEI 88

RESULT 7
US-10-667-295-42
; Sequence 42, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Mascia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(141)
; OTHER INFORMATION: Ceres Seq. ID no. 6425769
US-10-667-295-42

Query Match 10.8%; Score 58; DB 6; Length 141;
Best Local Similarity 23.3%; Pred. No. 3.6;
Matches 20; Conservative 10; Mismatches 24; Indels 32; Gaps 2;

Qy 8 AVLRAIDGINQRSSDANLYRLDLLDPRPTMGDPTPKPVSFYKVTVCPRTTQOSPDC 67
Db 74 SVVGAVDGV-----AMEVDVDSAK-----TNSNSDK 101

Qy 68 DPKKGLVKRCMGTVTLNQARGSPDI 93
Db 102 SEKDGRKRLCVGSQALNYRDRHMEI 127

RESULT 8
US-11-100-183-15
; Sequence 15, Application US/11100183
; Publication No. US2005027074A1
; GENERAL INFORMATION:
; APPLICANT: Stratagene California
; TITLE OF INVENTION: Compositions And Methods For Reverse Transcription
; FILE REFERENCE: 25436/2452
; CURRENT APPLICATION NUMBER: US/11/100,183
; CURRENT FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: US 60/559,810
; PRIOR FILING DATE: 2004-04-06
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 15
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Pasteurella multocida
US-11-100-183-15
```

| | | | | |
|-----------------------|--------------|---------------|----------------|-------------|
| Query Match | 10.6%; | Score 56.5; | DB 7; | Length 897; |
| Best Local Similarity | 30.9%; | Pred. No. 56; | | |
| Matches 17; | Conservative | 6; | Mismatches 23; | Indels 9; |
| | | | | Gaps 2; |

```

, GENERAL INFORMATION:
, APPLICANT: KIMMERY, WILLIAM JOHN
, TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
, FILE REFERENCE: PU3480US
, CURRENT APPLICATION NUMBER: US/10/793,626
, CURRENT FILING DATE: 2004-03-04
, PRIOR APPLICATION NUMBER: 60/164,258
, PRIOR FILING DATE: 1999-11-09
, NUMBER OF SEQ ID NOS: 4472
, SOFTWARE: PatentIn Ver. 2.1
, SEQ ID NO 566
, LENGTH: 244
, TYPE: PRT
, ORGANISM: Artificial Sequence
, FEATURE:
, OTHER INFORMATION: Description of Artificial Sequence: synthetic
, OTHER INFORMATION: amino acid sequence
US-10-793-626-566

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US-11-137-465-36
Query Match      10.6%; Score 56.5; DB 7; Length 993;
Best Local Similarity 30.9%; Pred. No. 64;
Matches 17; Conservative 6; Mismatches 23; Indels 9; Gaps 2;

Qy      46  PVSFYTKVETVCPRTTQOSPEDCDCKFDKGLVKRCMGVTTLNQARGSPDISCDKNK 100
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      263  PVGFMLQP---DRKTKCIDECRLNNGGCDHICRNTV-----GSPESCCKGYK 308

RESULT 12
US-11-113-424-37
; Sequence 37, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424

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; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 37
; LENGTH: 997
; TYPE: PRT
; ORGANISM: Mus musculus
; US-11-113-424-37

Query Match          10.6%; Score 56.5; DB 7; Length 997;
Best Local Similarity 30.9%; Pred. No. 64;
Matches 17; Conservative 6; Mismatches 23; Indels 9; Gaps 2;

Qy 46 PVSFTVKETVCPRTTQSPEDCDPKDGLVKRCMGTVTLNQARSGFIDCDKNK 100
Db 307 PTGFTLQ---VDGKTCQIDRCQTRNGCGNHFCKNTV-----GSFDCSCKKGFK 352

RESULT 13
US-10-467-657-7834
; Sequence 7834, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7834
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7834

Query Match          10.5%; Score 56; DB 6; Length 118;
Best Local Similarity 29.7%; Pred. No. 5;
Matches 19; Conservative 7; Mismatches 18; Indels 20; Gaps 4;

Qy 21 SDANLYRLDLLDPRMTDGP-----DTPKDVSTVKETVCPRTTQSPEDCDPKDGLV 75
Db 68 SSADLLRYRIQTAP-MFSEPPKTELDPKNVSFCSGTNCP-----APSD----- 112

Qy 76 KRCM 79
Db 113 NRCL 116

Search completed: January 12, 2006, 21:54:25
Job time : 4.47232 secs
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RESULT 14
US-10-793-626-2964
; Sequence 2964, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2964
; LENGTH: 5024
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
; FEATURES:
; NAME/KEY: MOD RES
; LOCATION: (5024)
; OTHER INFORMATION: variable amino acid
US-10-793-626-2964

Query Match          10.5%; Score 56; DB 6; Length 5024;
Best Local Similarity 34.2%; Pred. No. 5.6e+02;
Matches 13; Conservative 7; Mismatches 12; Indels 6; Gaps 1;

Qy 6 KEAVLRAIDGINQRSSDANLYRLDLLDPR-----PTM 37
Db 3196 KEIKQLTDAVNOANDLNGVELLDADKQNAHQSIPTL 3233

RESULT 15
US-10-995-561-878
; Sequence 878, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 878
; LENGTH: 729
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-878

Query Match          10.4%; Score 55.5; DB 6; Length 729;
Best Local Similarity 23.5%; Pred. No. 57;
Matches 23; Conservative 16; Mismatches 30; Indels 29; Gaps 3;

Qy 2 VLSYKEAVLRAIDGINQRSSDANLYRLDLLDPRMTDGPDPPTPKPVSTVKETVC----- 56
Db 363 LLGRKSSELDASD--SSSSSNLSLKV-----RPSSDLNNSGTQSPHHKQVRSVSSQK 415

Qy 57 -----PRTTQSPEDCDPKDGLVKR 77
Db 416 RRYSDHAGPAIPSVVAYPKRSQTSADSLKEDGISR 453

Search completed: January 12, 2006, 21:54:25
Job time : 4.47232 secs
```

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 12, 2006, 21:41:48 ; Search time 90.3321 Seconds
(without alignments)
826.886 Million cell updates/sec

Title: US-10-815-562-2
Perfect score: 879
Sequence: 1 MKTQDGHSLGRWSLVLLLL.....KRIQRIKDFLNLPRTES 170

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 879 | 100.0 | 170 | 3 | AAB07901 |
| 2 | 879 | 100.0 | 170 | 7 | AD18219 |
| 3 | 879 | 100.0 | 170 | 8 | AD129582 |
| 4 | 879 | 100.0 | 170 | 8 | AD182973 |
| 5 | 879 | 100.0 | 170 | 8 | AD182973 |
| 6 | 879 | 100.0 | 170 | 9 | AD182973 |
| 7 | 875 | 99.5 | 169 | 9 | AD182973 |
| 8 | 874 | 99.4 | 170 | 2 | AAR92924 |
| 9 | 874 | 99.4 | 170 | 2 | AAR92924 |
| 10 | 874 | 99.4 | 170 | 7 | AD182973 |
| 11 | 874 | 99.4 | 170 | 8 | AD182973 |
| 12 | 874 | 99.4 | 170 | 8 | AD182973 |
| 13 | 874 | 99.4 | 170 | 9 | AD182973 |
| 14 | 874 | 99.4 | 170 | 9 | AD182973 |
| 15 | 865 | 98.4 | 170 | 5 | AB07707 |
| 16 | 819 | 93.2 | 177 | 4 | AAU31061 |
| 17 | 761 | 86.6 | 152 | 3 | AAU31061 |
| 18 | 730 | 83.0 | 140 | 8 | AD182973 |
| 19 | 690 | 78.5 | 170 | 9 | AAU31061 |
| 20 | 493.5 | 56.1 | 172 | 9 | AD182973 |
| 21 | 468.5 | 53.3 | 171 | 5 | AB07707 |
| 22 | 457.5 | 52.0 | 170 | 5 | AAU31061 |
| 23 | 457.5 | 52.0 | 170 | 9 | AD182973 |
| 24 | 451 | 51.3 | 156 | 5 | AAU31061 |

| | | | | | |
|----|-------|------|-----|---|----------|
| 25 | 451 | 51.3 | 156 | 9 | AD182973 |
| 26 | 442.5 | 50.3 | 176 | 9 | AD182973 |
| 27 | 433.5 | 49.3 | 173 | 9 | AD182973 |
| 28 | 432 | 49.1 | 159 | 5 | AAU31061 |
| 29 | 432 | 49.1 | 159 | 5 | AAU31061 |
| 30 | 431.5 | 49.1 | 173 | 5 | AB07707 |
| 31 | 427.5 | 48.6 | 155 | 5 | AB07707 |
| 32 | 427.5 | 48.6 | 155 | 5 | AAU31061 |
| 33 | 427.5 | 48.6 | 155 | 5 | AAU31061 |
| 34 | 424.5 | 48.3 | 149 | 2 | AAW18157 |
| 35 | 421.5 | 48.0 | 172 | 9 | AD182973 |
| 36 | 418.5 | 47.6 | 147 | 2 | AAW18157 |
| 37 | 418.5 | 47.6 | 149 | 2 | AAW25081 |
| 38 | 418.5 | 47.6 | 149 | 2 | AAW18157 |
| 39 | 418.5 | 47.6 | 149 | 2 | AAW09087 |
| 40 | 418.5 | 47.6 | 149 | 2 | AAW18157 |
| 41 | 415.5 | 47.3 | 147 | 8 | AD18364 |
| 42 | 415.5 | 47.3 | 149 | 8 | AD18362 |
| 43 | 415.5 | 47.3 | 149 | 8 | AD18362 |
| 44 | 415.5 | 47.3 | 149 | 8 | AD18362 |
| 45 | 413 | 47.0 | 158 | 6 | ABP70875 |

ALIGNMENTS

| | | |
|----------|--|----------------------------|
| RESULT 1 | | |
| AAB07901 | | |
| ID | AAB07901 | standard; protein; 170 AA. |
| XX | | |
| XX | | |
| AC | AAB07901; | |
| XX | | |
| DT | 14-NOV-2000 | (first entry) |
| XX | | |
| DE | A human cationic protein designated CAP18. | |
| XX | | |
| KW | Human; cationic protein; lipopolysaccharide binding; anticoagulant; | |
| KW | CAP18; reactive nitrogen inhibitory protein; RNIP; gram negative sepsis; | |
| KW | coagulation-related disorder; disseminated intravascular coagulation. | |
| XX | | |
| OS | Homo sapiens. | |
| XX | | |
| Key | Location/Qualifiers | |
| FH | 134..170 | |
| FT | Protein | |
| FT | /note= "reactive nitrogen inhibitory protein" | |
| XX | | |
| PN | US6103888-A. | |
| XX | | |
| PD | 15-AUG-2000. | |
| XX | | |

PD - 4/2/03

314

CC designated CAP18. Amino acids 134-170 of CAP18 represent a reactive
 CC nitrogen inhibitory protein (RNIP). The CAP18 polynucleotide is useful
 CC for producing cationic proteins. The CAP18 polypeptide is useful for
 CC treating and diagnosing lipopolysaccharide-associated conditions such as
 CC gram negative sepsis, and/or coagulation-related disorders, such as
 CC disseminated intravascular coagulation

XX Sequence 170 AA;

Query Match 100.0%; Score 879; DB 3; Length 170;
 Best Local Similarity 100.0%; Pred. No. 4e-89;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTORHGSLGRWSLVLLLLGLVMPPLAIIAQLVLSYKEAVLRAIDGINORSSDANLYRLLD 60
 DB 1 MKTORHGSLGRWSLVLLLLGLVMPPLAIIAQLVLSYKEAVLRAIDGINORSSDANLYRLLD 60
 QY 61 LDPRTMDGDDPTPKPVSTVKTVCPRTTQSPEDCDFKDGKLVKRCMGTVTLNQARGS 120
 DB 61 LDPRTMDGDDPTPKPVSTVKTVCPRTTQSPEDCDFKDGKLVKRCMGTVTLNQARGS 120
 QY 121 FDISCDKDKRFPALLGDFPRKSKKIGKEFKRIVQRIKDFLRNLVPRTES 170
 DB 121 FDISCDKDKRFPALLGDFPRKSKKIGKEFKRIVQRIKDFLRNLVPRTES 170

RESULT 2

ADP18219
 ID ADF18219 standard; protein; 170 AA.

XX AC ADF18219;

XX DT 12-FEB-2004 (first entry)

XX DE Protein sequence.

XX KW Antimicrobial; LL-37; hCAP-18; antiarteriosclerotic; antiulcer;
 XX KW vulnerary; cytosstatic.

XX OS Unidentified.

XX FH Key Location/Qualifiers

XX FT Misc-difference 6 /note= "Encoded by AAT"

XX XX EPI358888-A1.

XX XX 05-NOV-2003.

XX XX 27-FEB-2003; 2003EP-00004306.

XX XX 28-FEB-2002; 2002EP-00004656.

XX XX (BALS/) BALS R.

XX XX (KOCZ/) KOCZULLA A R.

XX XX (VDEG/) VON DEGENFELD G.

XX XX Bals R, Koczulla AR, Von Degenfeld G;

XX XX WPI; 2003-879818/82.

XX XX N-PSDB; ADF18220.

XX XX Use of a peptide LL-37 for the preparation of a composition for
 PT preventing or treating wounds or a disease caused reduced blood flow,
 PT e.g. atherosclerosis, coronary heart disease, stroke, arterial occlusive
 PT diseases or ulcer.

XX PS Disclosure; Page; 15pp; English.

XX XX The present invention is based on the finding that human antimicrobial
 CC peptide LL-37 ADF18218 is capable of inducing functionally important
 CC angiogenesis in cell culture and in vivo by activation of the receptor
 CC molecule FPRL1. LL-37 can be used in the preparation of a pharmaceutical

CC composition for the prevention or treatment of a disease caused by, or
 CC resulting in, a reduced level of angiogenesis or arteriogenesis, or for
 CC the treatment of (infected) wounds or cancer. The disease may be
 CC associated with reduced blood flow, such as atherosclerosis, coronary
 CC heart disease, stroke, arterial occlusive disease or an ulcer.
 CC Suppression of angiogenesis through inhibition of LL-37 can be used to
 CC treat tumours, especially a carcinoma or sarcoma including cancer of the
 CC bile duct, brain, breast, colon, stomach, male and female reproductive
 CC organs, lung and airways, skin, gallbladder, liver, nasopharynx, nerve
 CC cells, kidney, prostate, and Kaposi's sarcoma (all claimed). The present
 CC protein sequence is not explained in the specification.

XX Sequence 170 AA;

Query Match 100.0%; Score 879; DB 7; Length 170;
 Best Local Similarity 100.0%; Pred. No. 4e-89;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTORHGSLGRWSLVLLLLGLVMPPLAIIAQLVLSYKEAVLRAIDGINORSSDANLYRLLD 60
 DB 1 MKTORHGSLGRWSLVLLLLGLVMPPLAIIAQLVLSYKEAVLRAIDGINORSSDANLYRLLD 60
 QY 61 LDPRTMDGDDPTPKPVSTVKTVCPRTTQSPEDCDFKDGKLVKRCMGTVTLNQARGS 120
 DB 61 LDPRTMDGDDPTPKPVSTVKTVCPRTTQSPEDCDFKDGKLVKRCMGTVTLNQARGS 120
 QY 121 FDISCDKDKRFPALLGDFPRKSKKIGKEFKRIVQRIKDFLRNLVPRTES 170
 DB 121 FDISCDKDKRFPALLGDFPRKSKKIGKEFKRIVQRIKDFLRNLVPRTES 170

RESULT 3

ADI29582

ID ADI29582 standard; protein; 170 AA.

XX AC ADI29582;

XX DT 22-APR-2004 (first entry)

XX DE Human CAP18, SEQ ID 4.

XX KW CAP18; cationic antimicrobial protein of 18 kDa; bacterial pneumonia;
 XX KW chronic lung disease; acute lung disease; inflammatory lung disease;
 XX KW ARDS; bronchial asthma; human.

XX OS Homo sapiens.

XX XX WO2004009640-A1.

XX XX 29-JAN-2004.

XX XX 22-JUL-2003; 2003WO-JP009267.

XX XX 22-JUL-2002; 2002JP-00213040.

XX XX 14-MAR-2003; 2003JP-00070932.

XX XX (SEK) SEIKAGAKU CORP.

XX XX Kirikae T, Toyooka K, Naiki Y, Tamura H, Ishizaka A, Hashimoto S;

XX XX WPI; 2004-143269/14.

XX XX New antibody against an antibacterial peptide, particularly human CAP18,
 PT applicable in reagents and kits for detection, diagnosis and monitoring
 PT of bacterial pneumonia.

XX PS Disclosure; SEQ ID NO 4; 52pp; Japanese.

XX XX The present invention relates to a novel CAP18 (cationic antimicrobial
 CC protein of 18 kDa) antibody that can bind with human CAP18 peptide
 CC fragments ADI29579-ADI29581. The antibody is useful in reagents and kits
 CC for the detection, diagnosis and monitoring bacterial pneumonia and other
 CC CAP18-related diseases like chronic and acute lung diseases, inflammatory

CC lung diseases, ARDS and bronchial asthma. The present sequence is human
 CC CAP18.
 CC
 SQ Sequence 170 AA;
 Query Match 100.0%; Score 879; DB 8; Length 170;
 Best Local Similarity 100.0%; Pred. No. 4e-89;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKTQDGHSLGRWSLVLLGLVMPLEIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
 Db 1 MKTQDGHSLGRWSLVLLGLVMPLEIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
 QY 61 LDPRPTMDGDDPTPKPVSVFTVKETVCPRTTQSPEDCDFKQDGLVKRCMGTVTLNQARGS 120
 Db 61 LDPRPTMDGDDPTPKPVSVFTVKETVCPRTTQSPEDCDFKQDGLVKRCMGTVTLNQARGS 120
 QY 121 FDISCDKDKNPALLGDFFRKSKEKIGKEFKRIVQRIKDFLRNLVPTRES 170
 Db 121 FDISCDKDKNPALLGDFFRKSKEKIGKEFKRIVQRIKDFLRNLVPTRES 170
 RESULT 4
 ADJ82973
 ID ADJ82973 standard; protein; 170 AA.
 AC ADJ82973;
 DT 06-MAY-2004 (first entry)
 XX Human Pep714-related peptide precursor SEQ ID NO: 1.
 DE pep714-related peptide; precursor; human; secreted peptide; Pep714;
 KW oral mucositis; oral lesion; cystic fibrosis; respiratory infection;
 KW pneumonia.
 XX Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..30
 FT /label= signal_peptide
 FT Protein 31..131
 FT /label= propeptide
 FT Cleavage-site 106..107
 FT /note= "dibasic peptidase cleavage site"
 FT Cleavage-site 130..131
 FT /note= "dibasic peptidase cleavage site"
 FT Protein 132..170
 FT /label= antibacterial_protein_FALL-39
 FT Protein 134..170
 FT /label= antibacterial_protein_LL-37
 FT Cleavage-site 140..141
 FT /note= "dibasic peptidase cleavage site"
 FT Cleavage-site 151..152
 FT /note= "dibasic peptidase cleavage site"
 FT
 FT
 FN WO2004005338-A1.
 XX
 XX 15-JAN-2004.
 XX
 XX 30-JUN-2003; 2003WO-EP006930.
 XX
 XX 08-JUL-2003; 2002US-0394486P.
 PR 07-JAN-2003; 2003US-0438602P.
 XX
 XX (GENE-) GENEPROT INC.
 XX Bougueleret L, Jeandenans C, Niknejad A;
 XX

DR WPI; 2004-099371/10.
 XX Novel Pep714-related polypeptide having biological activity, useful for
 PT treatment and prevention of microbial or viral infection, cystic fibrosis
 PT and chronic respiratory infections.
 XX Disclosure; Page 91-92; 99pp; English.
 XX The present invention relates to a Pep714-related peptide. This is useful
 CC for inhibiting microbial propagation, preferably viral propagation, and
 CC in the treatment of chemotherapy and radiotherapy induced oral mucositis,
 CC oral lesion, ventilator associated pneumonia, chronic respiratory
 CC infections and cystic fibrosis. The present sequence is a Pep714-related
 CC peptide precursor protein shown in the exemplification of the invention.
 XX
 SQ Sequence 170 AA;
 Query Match 100.0%; Score 879; DB 8; Length 170;
 Best Local Similarity 100.0%; Pred. No. 4e-89;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKTQDGHSLGRWSLVLLGLVMPLEIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
 Db 1 MKTQDGHSLGRWSLVLLGLVMPLEIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
 QY 61 LDPRPTMDGDDPTPKPVSVFTVKETVCPRTTQSPEDCDFKQDGLVKRCMGTVTLNQARGS 120
 Db 61 LDPRPTMDGDDPTPKPVSVFTVKETVCPRTTQSPEDCDFKQDGLVKRCMGTVTLNQARGS 120
 QY 121 FDISCDKDKNPALLGDFFRKSKEKIGKEFKRIVQRIKDFLRNLVPTRES 170
 Db 121 FDISCDKDKNPALLGDFFRKSKEKIGKEFKRIVQRIKDFLRNLVPTRES 170
 RESULT 5
 ADJ47315
 ID ADJ47315 standard; protein; 170 AA.
 XX ADJ47315;
 DT 18-NOV-2004 (first entry)
 XX Human cationic antimicrobial protein-18.
 DE Human cationic antimicrobial protein-18.
 KW cystic pulmonary fibrosis; cationic antimicrobial protein; CAP18;
 KW pulmonary disease.
 XX Homo sapiens.
 OS
 XX JP2004245842-A.
 PN 02-SEP-2004.
 PD
 XX 13-FEB-2004; 2004JP-00036471.
 PF
 XX 14-FEB-2003; 2003US-0447310P.
 PR
 XX (SEK) SEIKAGAKU KOGYO CO LTD.
 PA
 XX WPI; 2004-629858/61.
 DR
 XX Evaluating cystic pulmonary fibrosis, by measuring cationic antimicrobial
 PT protein of 18 kDa (CAP18) quantity in biological sample, and evaluating
 PT fibrosis by comparing measured quantity and quantity of CAP18 in control
 PT sample.
 XX Disclosure; SEQ ID NO 4; 14pp; Japanese.
 PS The invention relates to a novel method for evaluating cystic pulmonary
 CC fibrosis. The method comprises: measuring the quantity of cationic
 CC antimicrobial protein of 18 kDa (CAP18) in the biological sample
 CC collected from the individual; comparing the quantity of CAP18 measured
 CC in the previous step and the quantity of CAP18 in a control sample; and

CC evaluating cystic pulmonary fibrosis by associating comparison of
 CC obtained results. The invention further comprises: a kit for carrying out
 CC the evaluating method, comprising a solid-phase component and an antibody
 CC coupled with an antigenic peptide having a sequence of ABR47312, or a
 CC solid-phase component comprising an immobilised antibody (first antibody)
 CC which is coupled with the antigenic peptide, and the antibody (second
 CC antibody) coupled with the antigenic peptide. The method or kit are
 CC useful for evaluating cystic pulmonary fibrosis in an individual, where
 CC the evaluation includes diagnosis for the presence or absence of a risk
 CC of cystic pulmonary fibrosis, evaluation of serious or acute conditions,
 CC or the evaluation of the advanced grade of the disease. The method
 CC enables simple, cost-effective, rapid, highly sensitive and highly
 CC accurate evaluation of the acute or serious conditions, or the
 CC advancement of the pulmonary diseases. This sequence represents the human
 CC CAP18 protein of the invention.

XX Sequence 170 AA;
 SQ
 Query Match 100.0%; Score 879; DB 8; Length 170;
 Best Local Similarity 100.0%; Pred. No. 4e-89;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKTQRDGHSLGRWSLVLLLLGLVMPALIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
 DB 1 MKTQRDGHSLGRWSLVLLLLGLVMPALIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
 QY 61 LDPRTMDGDDPTPKPVSFTVKETVCPRTTQSPEDCDPKDGLVKRCMGTTLNQARGS 120
 DB 61 LDPRTMDGDDPTPKPVSFTVKETVCPRTTQSPEDCDPKDGLVKRCMGTTLNQARGS 120
 QY 121 FDISCDKDKRKFALLGDFPRKSKKEIGKPKRIVQRIKDFLNLVPRTES 170
 DB 121 FDISCDKDKRKFALLGDFPRKSKKEIGKPKRIVQRIKDFLNLVPRTES 170

RESULT 6
 ADW43827
 ID ADW43827 standard; peptide; 170 AA.
 AC ADW43827;
 XX
 DT 24-MAR-2005 (first entry)
 XX
 DE Mouse chemerin peptide SEQ ID NO 51.
 XX
 KW gene therapy; diagnosis; cell signaling; gene therapy;
 KW lymphoproliferative disease; dermatological disease; dermatological;
 KW hemostatic; inflammation; antinflammatory; hematological disease;
 KW immune disorder; neoplasm; cardiovascular-gen.; cns-gen.;
 KW neurological disease; hyperproliferative disorders; cytostatic; chemerin.
 XX
 OS Mus musculus.
 XX
 FN WO2005000875-A2.
 XX
 PD 06-JAN-2005.
 XX
 PF 25-JUN-2004; 2004WO-EP006945.
 XX
 PR 25-JUN-2003; 2003US-00603566.
 XX
 PA (EURO-) EUROSREEN SA.
 XX
 PI Wittamer V, Communi D, Dethoux M, Parmentier M, Loison C;
 PI Ooms FDR;
 XX
 DR WPI; 2005-058121/06.
 XX
 PT New Chemerin polypeptides, useful for diagnosing and treating a disease,
 PT e.g. neoplasms, hypergammaglobulinemia, paraproteinemia, purpura,
 PT sarcoidosis, Sezary Syndrome, Waldenström's Macroglobulinemia, Gaucher's
 PT Disease, or histiocytosis.
 XX
 XX

PS Example 2; SEQ ID NO 51; 183pp; English.
 XX
 CC The invention describes a polypeptide (I) of up to 50 amino acids where
 CC the polypeptide binds specifically to a chemerin polypeptide. Also
 CC described are: a nucleic acid sequence encoding (I); an expression vector
 CC comprising the coding sequence of the nucleic acid; a transgenic animal
 CC transformed with the expression vector; a (therapeutic) composition
 CC comprising (I) and an isolated Chemerin polypeptide or a nucleic acid
 CC sequence of (I); an antibody that selectively binds to (I); identifying
 CC an agent that modulates the interaction between a Chemerin polypeptide
 CC and a Chemerin polypeptide; detecting the presence, in a sample, of an
 CC agent that modulates the interaction between a Chemerin polypeptide and a
 CC Chemerin polypeptide in a sample; identifying an agent that modulates
 CC the function of Chemerin polypeptide; detecting the presence, in a
 CC sample, of an agent that modulates the function of Chemerin polypeptide;
 CC diagnosing a disease or disorder characterized by dysregulation of
 CC Chemerin (polypeptide) signaling; a kit, for screening agents that
 CC modulate the signaling activity of Chemerin polypeptide or for
 CC diagnosing a disease or disorder characterized by dysregulation of
 CC Chemerin polypeptide signaling, comprising an isolated Chemerin
 CC polypeptide, (I), an isolated polynucleotide encoding (I), a cell
 CC transformed with a polynucleotide encoding (I), and its packaging
 CC materials; a non-human mammal transgenic for a Chemerin polynucleotide
 CC encoding (I); identifying an antibody inhibiting Chemerin activation;
 CC and an in vitro method of inhibiting cell proliferation. The
 CC (therapeutic) composition or expression vector is useful for preparing a
 CC medicament for ex vivo gene therapy or for in vivo gene therapy or a
 CC medicament for inhibiting cell proliferation, where the medicament is
 CC used for treating a disease, e.g. neoplasms, hypergammaglobulinemia,
 CC lymphoproliferative diseases, disorders, and/or conditions,
 CC paraproteinemia, purpura, sarcoidosis, Sezary Syndrome, and any other
 CC Macroglobulinemia, Gaucher's disease, histiocytosis, and any other
 CC hyperproliferative disease. The polypeptides and polynucleotides and
 CC methods are useful for diagnosing and treating the cited diseases. This
 CC is the amino acid sequence of a mouse chemerin peptide used to analyse
 CC processing of immature chemerin.
 XX
 SQ Sequence 170 AA;

Query Match 100.0%; Score 879; DB 9; Length 170;
 Best Local Similarity 100.0%; Pred. No. 4e-89;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKTQRDGHSLGRWSLVLLLLGLVMPALIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
 DB 1 MKTQRDGHSLGRWSLVLLLLGLVMPALIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
 QY 61 LDPRTMDGDDPTPKPVSFTVKETVCPRTTQSPEDCDPKDGLVKRCMGTTLNQARGS 120
 DB 61 LDPRTMDGDDPTPKPVSFTVKETVCPRTTQSPEDCDPKDGLVKRCMGTTLNQARGS 120
 QY 121 FDISCDKDKRKFALLGDFPRKSKKEIGKPKRIVQRIKDFLNLVPRTES 170
 DB 121 FDISCDKDKRKFALLGDFPRKSKKEIGKPKRIVQRIKDFLNLVPRTES 170

RESULT 7
 ADK70797
 ID ADK70797 standard; protein; 169 AA.
 XX
 AC ADK70797;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Human CAP18 full-length protein.
 XX
 KW alpha-helix; thionine; antibacterial; antifungal; plant;
 KW fungi resistance; rice blast fungus; Ceratocystis fimbriata; bacteria;
 KW Pseudomonas; antimicrobial; rabbit; CAP18.
 XX
 OS Homo sapiens.
 XX
 PN JP2003204794-A.

XX PD 22-JUL-2003.
 XX PF 15-JAN-2002; 2002JP-00006607.
 XX PR 15-JAN-2002; 2002JP-00006607.
 XX PA (TOYU) TOYOTA CHUO KENKYUSHO KK.
 XX WPI; 2004-102620/11.
 XX Antimicrobial polypeptide composition for a plant pathogen, comprises one
 PT or more types of thionine and/or a polypeptide having an alpha helix
 PT structure, as an active ingredient.
 XX
 XX Disclosure; SEQ ID NO 38; 27pp; Japanese.
 XX The invention relates to a novel polypeptide composition for preventing
 CC disease in an organism which comprises one or more types of polypeptide
 CC which have an alpha-helix structure and/or thionine component. The
 CC composition of the invention demonstrates antibacterial and antifungal
 CC activities and may be useful for preventing a disease in an organism, for
 CC generating cultivated plants and in providing resistance to plant tissue
 CC against fungi such as *Pyricularia oryzae* (rice blast fungus),
 CC *Ceratocystis fimbriata* and bacteria such as *Pseudomonas* etc. The
 CC composition has high antimicrobial activity at low concentration. The
 CC current sequence is that of the rabbit CAP18 full-length protein of the
 CC invention.
 XX SQ Sequence 169 AA;
 Query Match 99.5%; Score 875; DB 8; Length 169;
 Best Local Similarity 100.0%; Pred. No. 1.1e-88;
 Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKTORHGSLGRWSLVLLGLVMPALIAQVLSYKEAVLRAIDGINORSSDANLYRLLD 60
 DB 1 MKTORHGSLGRWSLVLLGLVMPALIAQVLSYKEAVLRAIDGINORSSDANLYRLLD 60
 QY 61 LDPRFTMDGDDPTPKVSVFTVKETVCPRTTQOSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
 DB 61 LDPRFTMDGDDPTPKVSVFTVKETVCPRTTQOSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
 QY 121 FDISCDKDKNGKFPALLGDFFRKSKKEKIGKEFKRIVQRIKDFLNLYPRTES 169
 DB 121 FDISCDKDKNGKFPALLGDFFRKSKKEKIGKEFKRIVQRIKDFLNLYPRTES 169
 RESULT 8
 AAR92924
 ID AAR92924 standard; protein; 170 AA.
 XX AC AAR92924;
 XX DT 06-JUN-1996 (first entry)
 XX DE Prepro-FALL-99.
 XX KW FALL-39; cathelin; antibiotic; antimicrobial; antibacterial.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Peptide 1..131
 FT Protein /label= prepro-peptide
 FT 132..170
 FT /label= FALL-39
 XX WO9608508-A1.
 XX PD 21-MAR-1996.
 XX PF 12-SEP-1995; 95WO-S0001030.

XX PR 13-SEP-1994; 94SE-00003055.
 XX (BOMA/) BOWAN H G.
 XX PI Agerberth B, Gudmundsson GH, Gunne H;
 XX WPI; 1996-179899/18.
 DR N-PSDB; AAT18233.
 XX Novel peptide antibiotic, FALL-39 - overcomes classical antibiotic
 PT resistance and is non-cytotoxic.
 XX Example 2; Fig 1; 26pp; English.
 XX Novel cathelin-like prepro-FALL-39 (AAR92924) is the precursor of the
 CC antimicrobial, antibacterial agent FALL-39 (see AAR92923). It is the
 CC product of a cDNA clone (AAT18233) isolated from a human bone marrow cDNA
 CC library. FALL-39 includes a helical region (see AAR92922) that is
 CC required for biological activity. FALL-39 is useful therapeutically for
 CC inhibiting microbial growth in mammals, including humans, and is non-
 CC cytotoxic
 XX SQ Sequence 170 AA;
 Query Match 99.4%; Score 874; DB 2; Length 170;
 Best Local Similarity 99.4%; Pred. No. 1.4e-88;
 Matches 169; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKTORHGSLGRWSLVLLGLVMPALIAQVLSYKEAVLRAIDGINORSSDANLYRLLD 60
 DB 1 MKTORHGSLGRWSLVLLGLVMPALIAQVLSYKEAVLRAIDGINORSSDANLYRLLD 60
 QY 61 LDPRFTMDGDDPTPKVSVFTVKETVCPRTTQOSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
 DB 61 LDPRFTMDGDDPTPKVSVFTVKETVCPRTTQOSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
 QY 121 FDISCDKDKNGKFPALLGDFFRKSKKEKIGKEFKRIVQRIKDFLNLYPRTES 170
 DB 121 FDISCDKDKNGKFPALLGDFFRKSKKEKIGKEFKRIVQRIKDFLNLYPRTES 170
 RESULT 9
 AAU90996
 ID AAU90996 standard; peptide; 170 AA.
 XX AC AAU90996;
 XX DT 05-JUN-2002 (first entry)
 XX DE Transplant media associated antimicrobial peptide #32.
 XX KW Transplant; antimicrobial peptide; pore forming agent;
 KW cell surface receptor binding compound; kidney transplant; cardioplegia;
 KW organ transplant; transplant rejection.
 XX OS Homo sapiens.
 XX PN WO200209738-A1.
 XX PD 07-FEB-2002.
 XX PF 27-JUL-2001; 2001WO-US023785.
 XX PR 28-JUL-2000; 2000US-0221632P.
 PR 17-NOV-2000; 2000US-0249602P.
 PR 15-MAY-2001; 2001US-0290932P.
 XX (MURP/) MURPHY C J.
 XX PA Murphy CJ, Reid TW, Mcanulty JF;
 XX WPI; 2002-268995/31.

| | | |
|-----------|---|---|
| XX | | Media comprising antimicrobial polypeptides or pore forming agents and/or |
| PT | | cell surface receptor binding compounds useful for the storage and |
| PT | | preservation of organs prior to transplant. |
| XX | | |
| XX | | Disclosure; Page 27; 78pp; English. |
| PS | | |
| XX | | The invention describes new transplant compositions comprising |
| CC | | antimicrobial polypeptides or pore forming agents and/or cell surface |
| CC | | receptor binding compounds. The media is capable of extending the |
| CC | | preservation period past 72 hours and can provide organs with increased |
| CC | | functionality upon transplant. animals receiving kidneys stored in the |
| CC | | media of the present invention for either three or four days had serum |
| CC | | creatinine levels of less than half of those observed in control animals |
| CC | | receiving kidneys stored in UW solution (defined in the specification) |
| CC | | alone. Lower serum creatinine levels are indicative of healthier kidneys |
| CC | | and a more preferable prognosis for the transplant patient. The media of |
| CC | | the invention are useful for decreasing the incidence and/or severity of |
| CC | | delayed graft function in patients receiving transplanted kidneys stored |
| CC | | and/or treated in the media. The media may also be used in procedures |
| CC | | such as cardioplegia. It is contemplated that transplant of healthier |
| CC | | organs leads to a decrease in chronic rejection. This sequence represents |
| CC | | an antimicrobial peptide studied in the development of the transplant |
| CC | | media |
| XX | | |
| SQ | | Sequence 170 AA; |
| | Query Match | 99.4%; Score 874; DB 5; Length 170; |
| | Best Local Similarity | 99.4%; Pred. No. 1.4e-88; |
| | Matches 169; Conservative | 1; Mismatches 0; Indels 0; Gaps 0 |
| Qy | 1 | MKTQRDGHSLGRWSLVLLGLLGVNPLAIIAIVLSYKEAVLRADGINSRDANLYRLLD 60 |
| Db | 1 | MKTRNGHSLGRWSLVLLGLLGVNPLAIIAIVLSYKEAVLRADGINSRDANLYRLLD 60 |
| Qy | 61 | LDRPRTWDGDDPTPKVSVFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGVTTLNQARGS 120 |
| Db | 61 | LDRPRTWDGDDPTPKVSVFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGVTTLNQARGS 120 |
| Qy | 121 | FDISCDXDNKRFPALLGDFFRKSKEKGFKRIQRIKDPLRNLPRTES 170 |
| Db | 121 | FDISCDXDNKRFPALLGDFFRKSKEKGFKRIQRIKDPLRNLPRTES 170 |
| RESULT 10 | | |
| ADP65263 | | |
| ID | ADP65263 | standard; protein; 170 AA. |
| XX | AC | ADP65263; |
| XX | AC | |
| DT | 12-AUG-2004 | (first entry) |
| XX | | Human cathelicidin antimicrobial peptide. |
| DE | | |
| KW | | autoimmune disease; arthritis; gene expression analysis; |
| KW | | rheumatoid arthritis; collagen-induced; immunosuppressive; anticheumatic; |
| KW | | antiarthritis; osteopathic; antigout; antiinflammatory; dermatological; |
| KW | | immunomodulatory; lupus; ankylosing spondylitis; fibrositis; |
| KW | | fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis; |
| XX | | immune; human. |
| OS | | Homo sapiens. |
| XX | | |
| PN | WO2003072827-A1. | |
| XX | | |
| PD | 04-SEP-2003. | |
| XX | | |
| Pf | 31-OCT-2002; 2002WO-US035433. | |
| XX | | |
| PF | 31-OCT-2001; 2001US-0336220P. | |
| XX | | |
| PA | (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT. | |
| XX | | |

XX WO2004034061-A2.
 XX 22-APR-2004.
 XX 10-OCT-2003; 2003WO-EP011240.
 XX 10-OCT-2002; 2002GB-00023655.
 XX (MABT-) MABTECH AB.
 XX Boman H, Andersson M, Puetssep K, Carlsson G;
 XX WPI; 2004-364936/34.
 XX N-PSDB; ADN41826.
 XX Determination of susceptibility of subject to infection comprising
 XX detecting cathelicidin type peptide present in sample, optionally
 XX comparing level of peptide in sample to control sample.
 XX Disclosure; SEQ ID NO 2; 40pp; English.
 XX The present invention describes a method for determining the
 XX susceptibility of a subject to infection. The method comprises: (i)
 XX providing a sample from a subject; (ii) detecting any cathelicidin type
 XX peptide (LL-37) present in the sample; (iii) optionally comparing the
 XX level of LL-37 in the sample to a control sample; (iv) determining the
 XX susceptibility of the subject to infection (where no LL-37 or a low level
 XX of LL-37 indicates that subject is susceptible to infection); and (v)
 XX optionally administering an antimicrobial agent to reduce infection. Also
 XX described is a product containing LL-37 and a cytostatic drug,
 XX corticosteroid or growth factor (preferably recombinant granulocyte
 XX colony stimulating factor (G-CSF) or GM-CSF). The product has
 XX antimicrobial, antiinflammatory and immunostimulant activities. The
 XX method can be used for determining the susceptibility of a subject to
 XX infection such as bacterial infection (e.g. Actinobacillus
 XX actinomycetemcomitans infection) and neutropenia, and for diagnosing
 XX neutropenia (e.g. Kostmann morbus). The method is also useful in the
 XX manufacture of a medicament in the form of toothpaste or mouthwash for
 XX the preventative treatment of infection e.g. gingivitis, oral infection
 XX (such as periodontitis), and for the treatment of neutropenia. The method
 XX controls the normal flora in neutropenia and so combat infections. The
 XX present sequence represents the proform of human LL-37, which is used in
 XX the exemplification of the present invention.
 XX Sequence 170 AA;
 XX Query Match 99.4%; Score 874; DB 8; Length 170;
 XX Best Local Similarity 99.4%; Pred. No. 1.4e-88;
 XX Matches 169; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKTORGHSLGRWSLVLLLLGLVMPALIAQVLSYKEAVLRAIDGINORSSDANLYRLLD 60
 Db 1 MKTORGHSLGRWSLVLLLLGLVMPALIAQVLSYKEAVLRAIDGINORSSDANLYRLLD 60
 QY 61 LDPRTMDGDDPTPKPVSVFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGVTTLNQARGS 120
 Db 61 LDPRTMDGDDPTPKPVSVFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGVTTLNQARGS 120
 QY 121 FDISCDKDKNGKRFALLGDFFRKSKGKIGKFKRIVQRIKDFLRLNLPRTES 170
 Db 121 FDISCDKDKNGKRFALLGDFFRKSKGKIGKFKRIVQRIKDFLRLNLPRTES 170
 RESULT 12
 ABM80449
 ID ABM80449 standard; protein; 170 AA.
 XX ABM80449;
 XX AC
 XX 18-NOV-2004 (first entry)
 DE Tumour-associated antigenic target (TAT) polypeptide PRO36373, SEQ:1129.

XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;
 KW tumour; diagnosis; cell proliferative disorder; breast cancer;
 KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
 KW central nervous system cancer; bladder cancer; pancreatic cancer;
 KW cervical cancer; melanoma; leukaemia; hybridisation probe;
 KW chromosome identification; chromosome mapping; gene mapping;
 XX gene therapy; cytostatic.
 XX Homo sapiens.
 XX OS
 XX WO2004030615-A2.
 XX 15-APR-2004.
 XX 29-SEP-2003; 2003WO-US028547.
 XX 02-OCT-2002; 2002US-0414971P.
 XX (GETH) GENENTECH INC.
 XX Wu TD, Zhang Z, Zhou Y;
 XX WPI; 2004-347921/32.
 XX N-PSDB; ACN37923.
 XX New tumor-associated antigenic target polypeptides and nucleic acids,
 XX useful in preparing a medicament for treating or detecting a
 XX proliferative disorder, e.g. breast, lung, colorectal, ovarian or
 XX prostate cancer or tumor.
 XX Claim 12; SEQ ID NO 1129; 7273pp; English.
 XX The invention relates to human tumour-associated antigenic target (TAT)
 XX polypeptides, and their related nucleic acids. The TAT polypeptides are
 XX overexpressed in cancer tissues compared to normal tissues, and may thus
 XX serve as effective targets for the diagnosis and treatment of cancer in
 XX mammals. The invention also relates to nucleic acid and polypeptide
 XX sequences at least 80% identical to the TAT nucleic acids and
 XX polypeptides; expression vectors and host cells comprising a TAT nucleic
 XX acid; an antibody specific for a TAT polypeptide; a peptide or organic
 XX molecule which binds to a TAT polypeptide; fusion proteins comprising a
 XX TAT polypeptide; and methods and compositions for the treatment or
 XX diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
 XX antibodies, antagonists, binding molecules and compositions are useful
 XX for diagnosing or treating a cell proliferative disorder associated with
 XX increased TAT expression, particularly cancers such as breast cancer,
 XX colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
 XX cancer, pancreatic cancer, cervical cancer, cancers of the central
 XX nervous system, melanoma and leukaemia. TAT nucleic acids may further be
 XX used as hybridisation probes, in chromosome and gene mapping, in
 XX chromosome identification and in gene therapy. The present sequence
 XX represents a TAT polypeptide of the invention
 XX Sequence 170 AA;
 XX Query Match 99.4%; Score 874; DB 8; Length 170;
 XX Best Local Similarity 99.4%; Pred. No. 1.4e-88;
 XX Matches 169; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKTORGHSLGRWSLVLLLLGLVMPALIAQVLSYKEAVLRAIDGINORSSDANLYRLLD 60
 Db 1 MKTORGHSLGRWSLVLLLLGLVMPALIAQVLSYKEAVLRAIDGINORSSDANLYRLLD 60
 QY 61 LDPRTMDGDDPTPKPVSVFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGVTTLNQARGS 120
 Db 61 LDPRTMDGDDPTPKPVSVFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGVTTLNQARGS 120
 QY 121 FDISCDKDKNGKRFALLGDFFRKSKGKIGKFKRIVQRIKDFLRLNLPRTES 170
 Db 121 FDISCDKDKNGKRFALLGDFFRKSKGKIGKFKRIVQRIKDFLRLNLPRTES 170

```

RESULT 13
ADX08374
ID ADX08374 standard; protein; 170 AA.
XX
XX
AC ADX08374;
XX
XX 21-APR-2005 (first entry)
XX
XX Cathelicidin antimicrobial peptide SEQ ID NO 47.
XX
XX vulnery; antiulcer; antiinflammatory; gastrointestinal-gen.;
XX expression; vector; wound healing; vulnery; injury; antimicrobial.
XX
XX Homo sapiens.
XX
XX WO2005012492-A2.
XX
XX 10-FEB-2005.
XX
XX 30-JUL-2004; 2004WO-US024627.
XX
XX 01-AUG-2003; 2003US-0491869P.
XX
XX 08-AUG-2003; 2003US-0493664P.
XX
XX 30-JUL-2004; 51US-00493664.
XX
XX (STRA-) STRATATECH CORP.
XX
XX Centanni JM, Allen-Hoffmann L;
XX
XX WPI; 2005-142888/15.
XX
XX Providing cells expressing heterologous keratinocyte growth factor-2 (I),
XX which is useful to treat wounds e.g. ulcerative colitis, comprises
XX introducing a vector comprising a DNA that encodes (I) to a host cell and
XX culturing the host cell.
XX
XX Disclosure; SEQ ID NO 47; 116pp; English.
XX
XX The invention describes providing cells expressing heterologous
XX keratinocyte growth factor-2 (KGF-2) (I) comprising providing a host cell
XX (II) consisting of primary keratinocytes and immortalized keratinocytes
XX and an expression vector comprising a DNA sequence encoding (I) operably
XX linked to a regulatory sequence; introducing the expression vector to
XX (II); and culturing (II) under conditions such that (I) is expressed.
XX Also described are: (II) produced by the novel method; a composition
XX comprising (II) expressing (I); a method of treating wounds; a vector
XX comprising a keratinocyte specific promoter operably linked to a DNA
XX sequence encoding KGF-2 or an antimicrobial polypeptide; a host cell
XX comprising the vector; a human tissue comprising the host cell, which
XX comprises the vector; a method for providing a skin equivalent expressing
XX an exogenous antimicrobial polypeptide; a composition comprising
XX keratinocytes expressing an exogenous antimicrobial polypeptide; a method
XX for providing a human tissue expressing an exogenous KGF-2 and an
XX exogenous antimicrobial polypeptide; a method of selecting cells with
XX increased pluripotency or multipotency relative to a population
XX comprising providing a population of cells and electroporating the cells
XX under conditions such that electroporated cells with increased
XX pluripotency or multipotency relative to the population of cells are
XX selected; a population of cells generated by the method; a population of
XX cells generated by the method; a method of selecting keratinocytes with
XX holoclone or meroclone cell morphology comprising providing a population
XX of keratinocytes and electroporating the keratinocytes under conditions
XX such that electroporated keratinocytes with holoclone or meroclone cell
XX morphology are selected; and a keratinocyte population generated by the
XX method. (I) is useful to treat wounds such as venous ulcers, diabetic
XX ulcers, pressure ulcers, burns, ulcerative colitis, mucosal injuries,
XX internal injuries or external injuries. The method is useful to increase
XX practitioners's success in healing wounds and/or accelerate the rate of
XX chronic wound healing. The NIKS cells is genetically uniform, pathogen
XX free human keratinocytes. This is the amino acid sequence of an
XX antimicrobial peptide of the invention.
XX
XX Sequence 170 AA;

```

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Query Match          99.4%; Score 874; DB 9; Length 170;
Best Local Similarity 99.4%; Pred. No. 1.4e-88;
Matches 169; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTORDGHSLSVLLGLVMPPLAIIAQLVSYKEAVLRAIDGINORSSDANLYRLLD 60
   |||||:|||||
Db 1 MKTONGHSLGRWSLVLLGLVMPPLAIIAQLVSYKEAVLRAIDGINORSSDANLYRLLD 60
   |||||:|||||
QY 61 LDPPTMDGDDPTPKPVSTVKETVCPRTTQOSPEDCDFKKGVLVRCMGVTVTLNQARGS 120
   |||||:|||||
Db 61 LDPPTMDGDDPTPKPVSTVKETVCPRTTQOSPEDCDFKKGVLVRCMGVTVTLNQARGS 120
   |||||:|||||
QY 121 FDISCDKDKRFPALLGDFFRKSKGKIKGFKRIQRIKDFLRNLVPRTES 170
   |||||:|||||
Db 121 FDISCDKDKRFPALLGDFFRKSKGKIKGFKRIQRIKDFLRNLVPRTES 170
   |||||:|||||

RESULT 14
ADZ80363
ID ADZ80363 standard; protein; 170 AA.
XX
AC ADZ80363;
XX
XX 14-JUL-2005 (first entry)
XX
XX Human cathelicidin polypeptide.
XX
XX Infection; viral infection; cathelicidin; atopic dermatitis;
XX antimicrobial; virucide; dermatological; dermatological disease;
XX immune disorder; inflammation.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Misc-difference 6 /note= "Encoded by GAT"
XX
XX WO2005040201-A1.
XX
XX 06-MAY-2005.
XX
XX 20-OCT-2004; 2004WO-US034948.
XX
XX 21-OCT-2003; 2003US-0512953P.
XX
XX (REGC ) UNIV CALIFORNIA.
XX (NAJFE-) NAT JEWISH MEDICAL & RES CENT.
XX
XX Gallo R, Murakami M, Leung DYM;
XX
XX WPI; 2005-355820/36.
XX N-PSDB; ADZ80362.
XX
XX Inhibiting spread and/or reducing risk of infection of virus, involves
XX contacting virus with cathelicidin functional fragment.
XX
XX Disclosure; SEQ ID NO 6; 78pp; English.
XX
XX The invention relates to a method of inhibiting the spread and/or
XX reducing the risk of infection of a virus, involving contacting a virus
XX with a cathelicidin functional fragment. The invention also relates to a
XX method of treating atopic dermatitis involving contacting a subject
XX having or suspected of having atopic dermatitis with an inhibiting
XX effective amount of a cathelicidin functional fragment. The cathelicidin
XX functional fragment comprises a peptide with antimicrobial and/or
XX antiviral activity. The methods are useful for inhibiting the spread
XX and/or reducing the risk of infection of a virus and for treating atopic
XX dermatitis. This sequence represents the human cathelicidin polypeptide
XX of the invention.
XX
XX Sequence 170 AA;

```

Query Match 99.4%; Score 874; DB 9; Length 170;
 Best Local Similarity 99.4%; Pred. No. 1.4e-88;
 Matches 169; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTQDGHSLGRWSLVLLGLVMPPLAIITAOVLSYKEAVLRAIDGINORSSDANLYRLLD 60
 DB 1 MKTQDGHSLGRWSLVLLGLVMPPLAIITAOVLSYKEAVLRAIDGINORSSDANLYRLLD 60
 QY 61 LDPRTMDGDDPTPKPVSFTVKETVCPRTTQOSPEDCDPKDGLVKRCMGTVTLNOARGS 120
 DB 61 LDPRTMDGDDPTPKPVSFTVKETVCPRTTQOSPEDCDPKDGLVKRCMGTVTLNOARGS 120
 QY 121 FDISCDKDKRFPALLGDFPRKSKKEKIGKFKRIVQRIKDFLNLVPTES 170
 DB 121 FDISCDKDKRFPALLGDFPRKSKKEKIGKFKRIVQRIKDFLNLVPTES 170

RESULT 15
 ABB07707
 ID ABB07707 standard; peptide; 170 AA.
 AC ABB07707;
 DT 10-JUN-2002 (first entry)
 DE Human peptide antibiotic FALL-39 precursor sequence.
 XX Vaccine; cathelicidin; antimicrobial; immunostimulant; immune response;
 KW antigen presenting cell; adjuvant; human; antibiotic; FALL-39.
 XX Homo sapiens.
 OS
 XX
 PN WO200213857-A2.
 XX
 PD 21-FEB-2002.
 XX
 PF 17-AUG-2001; 2001WO-EP009529.
 XX
 PR 17-AUG-2000; 2000AT-00001416.
 XX
 PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
 XX
 PI Fritz J, Mattner F, Zauner W, Buschle M, Egyed A;
 XX
 DR WPI; 2002-269154/31.
 XX
 PT Vaccine for active immunization or for preparing an adjuvant for
 PT enhancing an immune response to at least one antigen, comprises at least
 PT one antigen and at least one cathelicidin derived antimicrobial peptide.
 PS
 XX Disclosure; Fig 1; 65pp; English.
 CC The invention relates to a vaccine comprising at least one antigen and at
 CC least one cathelicidin derived antimicrobial peptide or its derivative.
 CC The vaccine is useful for active immunization, especially of humans or
 CC animals without protection against the specific antigen. The cathelicidin
 CC derived antimicrobial peptide is useful in the preparation of an adjuvant
 CC for enhancing the immune response to at least one antigen, where the
 CC adjuvant enhances the uptake of at least one antigen in antigen
 CC presenting cells (APC), and the adjuvant is added to the vaccine.
 CC Sequences ABB07701-07 represent cathelicidin proteins from various
 CC species
 XX
 SQ Sequence 170 AA;

Query Match 98.4%; Score 865; DB 5; Length 170;
 Best Local Similarity 98.8%; Pred. No. 1.4e-87;
 Matches 168; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKTQDGHSLGRWSLVLLGLVMPPLAIITAOVLSYKEAVLRAIDGINORSSDANLYRLLD 60
 DB 1 MKTQDGHSLGRWSLVLLGLVMPPLAIITAOVLSYKEAVLRAIDGINORSSDANLYRLLD 60

QY 61 LDPRTMDGDDPTPKPVSFTVKETVCPRTTQOSPEDCDPKDGLVKRCMGTVTLNOARGS 120
 DB 61 LDPRTMDGDDPTPKPVSFTVKETVCPRTTQOSPEDCDPKDGLVKRCMGTVTLNOARGS 120
 QY 121 FDISCDKDKRFPALLGDFPRKSKKEKIGKFKRIVQRIKDFLNLVPTES 170
 DB 121 FDISCDKDKRFPALLGDFPRKSKKEKIGKFKRIVQRIKDFLNLVPTES 170

Search completed: January 12, 2006, 21:48:09
 Job time : 92.3321 secs

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OM protein - protein search, using sw model

Run on: January 12, 2006, 21:43:14 ; Search time 15.0554 Seconds
(without alignments)
1086.448 Million cell updates/sec

Title: US-10-815-562-2

Perfect score: 879

Sequence: 1 MKTQRDGHSLGRWSLVLLLL.....KRIVQRIKDFLNLVPRTES 170

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 879 | 100.0 | 170 | 2 138932 | CAP18 precursor - |
| 2 | 874 | 99.4 | 170 | 2 S74248 | antibacterial pept |
| 3 | 465.5 | 53.0 | 171 | 2 J01171 | 18K lipopolysaccha |
| 4 | 444.5 | 50.6 | 167 | 2 S88967 | antibacterial pept |
| 5 | 443.5 | 50.5 | 166 | 2 S41731 | antibacterial prot |
| 6 | 438.5 | 49.9 | 153 | 2 A53421 | antibacterial pept |
| 7 | 432.5 | 49.2 | 155 | 2 S68229 | antimicrobial pept |
| 8 | 431.5 | 49.1 | 173 | 2 S70521 | cathelin-related p |
| 9 | 429.5 | 48.9 | 228 | 2 S40463 | prophenin (PR-2) p |
| 10 | 427.5 | 48.6 | 155 | 2 S27018 | bactenecin precurs |
| 11 | 427.5 | 48.6 | 172 | 2 S68232 | antimicrobial prot |
| 12 | 424.5 | 48.3 | 149 | 2 S57609 | protegrin 5 precu |
| 13 | 418.5 | 47.6 | 147 | 2 JN0900 | protegrin 2 precu |
| 14 | 418.5 | 47.6 | 149 | 2 A53895 | protegrin 3 precu |
| 15 | 418.5 | 47.6 | 149 | 2 S57607 | protegrin 1 precu |
| 16 | 418.5 | 47.6 | 149 | 2 B53895 | protegrin 4 precu |
| 17 | 410.5 | 46.7 | 176 | 2 A45328 | bactenecin 5 precu |
| 18 | 406 | 46.2 | 160 | 2 S68412 | indolicidin precu |
| 19 | 405.5 | 46.1 | 144 | 1 JC1222 | indolicidin precu |
| 20 | 399 | 45.4 | 160 | 2 S68228 | myeloid antimicrob |
| 21 | 396 | 45.1 | 152 | 2 S68411 | cathelin-related p |
| 22 | 387.5 | 44.1 | 212 | 2 S7330 | cathelin-like anti |
| 23 | 374.5 | 42.6 | 190 | 2 S68230 | antimicrobial pept |
| 24 | 319 | 36.3 | 96 | 1 XKPGC | cathelin - pig |
| 25 | 172.5 | 19.6 | 135 | 2 B46634 | polymorphonuclear |
| 26 | 171.5 | 19.5 | 137 | 2 A46634 | secreted phosphopr |
| 27 | 85.5 | 9.7 | 200 | 2 I46051 | kininogen, LMW II |
| 28 | 85 | 9.7 | 434 | 1 KGBOL2 | kininogen, LMW II |
| 29 | 85 | 9.7 | 619 | 1 KGBOL2 | kininogen, LMW II |

| | | | | | |
|----|------|-----|------|----------|---------------------|
| 30 | 84 | 9.6 | 436 | 1 KGBOL1 | kininogen, LMW I p |
| 31 | 84 | 9.6 | 621 | 1 KGBOL1 | kininogen, LMW I p |
| 32 | 82.5 | 9.4 | 273 | 2 AC1435 | hypothetical prote |
| 33 | 82 | 9.3 | 211 | 2 G01654 | spp-24 precursor - |
| 34 | 79 | 9.0 | 263 | 2 C84397 | hypothetical prote |
| 35 | 79 | 9.0 | 923 | 2 A53054 | lipoxxygenase (EC 1 |
| 36 | 78.5 | 8.9 | 445 | 2 T50802 | serine/threonine p |
| 37 | 78.5 | 8.9 | 1082 | 2 T31112 | ATPase 2 (EC 3.6.1 |
| 38 | 77.5 | 8.8 | 444 | 2 T18804 | hypothetical prote |
| 39 | 77 | 8.8 | 518 | 2 S44637 | f22b7.6 protein - |
| 40 | 77 | 8.8 | 532 | 2 H84123 | CTP synthetase ctr |
| 41 | 77 | 8.8 | 2911 | 2 T20566 | hypothetical prote |
| 42 | 76.5 | 8.7 | 245 | 2 F84680 | hypothetical prote |
| 43 | 75 | 8.5 | 505 | 2 F95345 | FixL Oxygen regula |
| 44 | 75 | 8.5 | 505 | 2 S39984 | nitrogen fixation |
| 45 | 75 | 8.5 | 1599 | 2 T15854 | hypothetical prote |

ALIGNMENTS

RESULT 1

I38932

CAP18 precursor - human

C/Species: Homo sapiens (man)

C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004

C/Accession: I38932

R/Larick, J.W.; Hirata, M.; Balint, R.F.; Lee, J.; Zhong, J.; Wright, S.C.

Infect. Immun. 63, 1291-1297, 1995

A/Title: Human CAP18: a novel antimicrobial lipopolysaccharide-binding protein.

A/Reference number: I38932; MUID:95197251; PMID:7890387

A/Accession: I38932

A/Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: mRNA

A/Residues: 1-170 <RES>

A/Cross-references: UNIPROT:P49913; UNIPARC:UPI0000000A67; EMBL:U19970; NID:G643476; PID

A/Superfamily: cathelin; cystatin homology

F:22-130/Domain: cystatin homology <CYS>

Query Match 100.0%; Score 879; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 8.8e-77;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | | |
|----|-----|---------------------------|-----------------------------------|-----|
| Qy | 1 | MKTQRDGHSLGRWSLVLLLLGLVMP | LAIIAQVLSYKEAVLRAIDGINRSDANLYRLLD | 60 |
| Db | 1 | MKTQRDGHSLGRWSLVLLLLGLVMP | LAIIAQVLSYKEAVLRAIDGINRSDANLYRLLD | 60 |
| Qy | 61 | LDPRPTWDGDDPTPKPVSTFKETVC | PTTQOSPEDCDPKDGLVKRCMGTTVLNQARGS | 120 |
| Db | 61 | LDPRPTWDGDDPTPKPVSTFKETVC | PTTQOSPEDCDPKDGLVKRCMGTTVLNQARGS | 120 |
| Qy | 121 | FDISCDKDKRFPALLGDPFFRKSKE | KIGKEFKRIQRIKDFLNLVPRTES | 170 |
| Db | 121 | FDISCDKDKRFPALLGDPFFRKSKE | KIGKEFKRIQRIKDFLNLVPRTES | 170 |

RESULT 2

S74248

antibacterial peptide LL-37 precursor - human

N/Alternate names: antibacterial peptide FALL39

N/Contains: antibacterial peptide LL-37; cathelin-related antibacterial peptide CAP-18

C/Species: Homo sapiens (man)

C/Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 09-Jul-2004

C/Accession: S74248; S78211; S66281; S66205; A55596; S49441; S58023

R/Gudmundsson, G.H.; Agerberth, B.; Odeberg, J.; Bergman, T.; Olsson, B.; Salcedo, R.

Eur. J. Biochem. 238, 325-332, 1996

A/Title: The human gene FALL39 and processing of the cathelin precursor to the antibacte

A/Reference number: S74248; MUID:96283824; PMID:8681941

A/Accession: S74248

A/Molecule type: DNA

A/Residues: 1-170 <GUD>

A/Cross-references: UNIPROT:P49913; UNIPARC:UPI0000017636C; EMBL:X96735

A/Accession: S78211

Db 118 FDLSCHNEFGNQPRFKISRLAGLLRKGGEKIKGKLNFKQLVPPQE 172

RESULT 9

S40463

prophenin (PF-2) precursor - pig

N;Alternate names: antimicrobial peptide; cathelin-like antibacterial peptide p

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 09-Jul-2004

C;Accession: S40463; S57331; S68233

P;Pungarcar, J.; Strukelj, B.; Kopitar, G.; Renko, M.; Lenarcic, B.; Gubensek,

FEBS Lett. 336, 284-288, 1993

A;Title: Molecular cloning of a putative homolog of proline/arginine-rich antib

A;Reference number: S40463; MUID:94085623; PMID:8462247

A;Accession: S40463

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-228 <PUN>

F;144-155/Product: bactenecin #status experimental <WAT>
F;146-154/Disulfide bonds: #status experimental

| | | | | | | | | | |
|-----------------------|-------|--------------|---------|------------|--------|--------|---|------|---|
| Query Match | 48.6% | Score | 427.5 | DB 2 | Length | 155 | | | |
| Best Local Similarity | 66.7% | Pred. No. | 1.4e-33 | | | | | | |
| Matches | 84 | Conservative | 18 | Mismatches | 23 | Indels | 1 | Gaps | 1 |

QY 1 MKTORGHSLGRWSLVLLLLGLVMPALIAITQVLSYKEAVLRAIDGINSORSSDANLYRLLD 60
Db 1 METPRASLSLGRWSLVLLLLGLALPSA-SQAALSYSREAVLRAVDQLNQESSEFNIVRLLE 59
QY 61 LDRPRPTMDGDDPTPKVSVFTVKETVCPRTTQOSPECDKFCGLVKRCMGTVTLTNQARGS 120
Db 60 LDQPPQDDEDPSPKRSVRVKETVCSRTTQPPQCDKFENGLLRKCEGTVTLDDQVRGN 119
QY 121 FDISCD 126
Db 120 FDIITCN 125

RESULT 11
S68232
antimicrobial protein PR-39 precursor, cathelin-associated - pig
N;Alternate names: myeloid antibacterial protein PR-39
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S68232; JN0899; I47138; S19563
R;Zhao, C.; Ganz, T.; Lehrer, R.I.
FEBS Lett. 376, 130-134, 1995
A;Title: Structures of genes for two cathelin-associated antimicrobial peptides
A;Reference number: S68232; MUID:96105365; PMID:7498526
A;Accession: S68232
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-172 <ZHA>
A;Cross-references: UNIPROT:P80054; UNIPARC:UPI000013215A; EMBL:X89201; NID:g11
A;Experimental source: leukocytes
R;Storici, P.; Zanetti, M.
Biochem. Biophys. Res. Commun. 196, 1058-1065, 1993
A;Title: A cDNA derived from pig bone marrow cells predicts a sequence identical
A;Reference number: JN0899, MUID:94071853; PMID:8250863
A;Accession: JN0899
A;Molecule type: mRNA
A;Residues: 1-20, 'A', 22-172 <STO>
A;Cross-references: UNIPARC:UPI000016C6E7; GB:L23825; NID:g435100; PIDN:AAA3110
R;Gudmundsson, G.H.; Magnusson, K.P.; Chowdhary, B.P.; Johansson, M.; Andersson
Proc. Natl. Acad. Sci. U.S.A. 92, 7085-7089, 1995
A;Title: Structure of the gene for porcine peptide antibiotic PR-39, a cathelin
A;Reference number: I47138; MUID:95350216; PMID:7624374
A;Accession: I47138
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-28, 'T', 30-89, 'QR', 92-116, 'NDP', 120-172 <GUD>
R;Agerberth, B.; Lee, J.Y.; Bergman, T.; Carlquist, M.; Boman, H.G.; Mutt, V.;
Eur. J. Biochem. 202, 849-854, 1991
A;Title: Amino acid sequence of PR-39. Isolation from pig intestine of a new mouse
A;Reference number: S19563; MUID:92111534; PMID:1765098
A;Accession: S19563
A;Molecule type: protein
A;Residues: 131-169 <AGE>
A;Cross-references: UNIPARC:UPI000002D613
A;Experimental source: intestine
C;Genetics: PR39
A;Gene: PR39
A;Introns: 66/3; 102/3; 126/3
C;Superfamily: cathelin; cystatin homology
C;Keywords: amidated carboxyl end; antibacterial
F;1-29/Domain: signal sequence #status predicted <SIG>
F;22-129/Domain: cystatin homology <CYS>
F;30-130/Domain: propeptide #status predicted <PRO>
F;131-169/Product: antimicrobial protein PR-39 #status experimental <WAT>

A;Reference number: JN0900; MUID:94071898; PMID:8250892
A;Accession: JN0900
A;Molecule type: mRNA
A;Residues: 1-147 <STO>
A;Cross-references: UNIPROT:P32195; UNIPARC:UPI0000131776; GB:L24745; NID:9431435; PIDN:
R;Mirgorodskaya, O.A.; Shevchenko, A.A.; Abdalla, K.O.M.A.; Chernushevich, I.V.; Egorov,
FEBS Lett. 330, 339-342, 1993
A;Title: Primary structure of three cationic peptides from porcine neutrophils. Sequence
A;Reference number: S36820; MUID:93387466; PMID:8375505
A;Accession: S36822
A;Molecule type: protein
A;Residues: 131-146 <MIR>
A;Cross-references: UNIPARC:UPI000014310F
R;Kokryakov, V.N.; Harwig, S.S.L.; Panyutich, E.A.; Shevchenko, A.A.; Alekhina, G.M.; Sh
FEBS Lett. 327, 231-236, 1993
A;Title: Protegrins: leukocyte antimicrobial peptides that combine features of corticost
A;Reference number: S34585; MUID:93327946; PMID:8335113
A;Accession: S34586
A;Molecule type: protein
A;Residues: 131-146 <KOK>
A;Cross-references: UNIPARC:UPI000014310F
C;Comment: This protein plays a role in the nonoxidative antimicrobial defense mechanism
C;Superfamily: cathelin; cystatin homology
C;Keywords: amidated carboxyl end; antibacterial; neutrophil
F;1-29/Domain: signal sequence \$status predicted <SIG>
F;22-129/Domain: cystatin homology <CYS>
F;131-146/Product: protegrin 2 \$status experimental <MAT>
F;146/Modified site: amidated carboxyl end (Val) (amide in mature form from following gl

Query Match 47.6%; Score 418.5; DB 2; Length 147;
Best Local Similarity 65.4%; Pred. No. 9.3e-33;
Matches 83; Conservative 19; Mismatches 24; Indels 1; Gaps 1;
QY 1 MKTORDGHSIGRWSLVLLLLGLVMPALIAIQVLVSYKEAVLRALDGINQRRSDANLYRLLD 60
Db 1 METQPSASLCIGRWSLWLLLLLALVPSA-SAQAALSYREAVLRVDRNLNEQSSEANLYRLLE 59
QY 61 LDRPRTWMDGDPDPKPVSFYTKVETCPRTTQSPEDCDFPKQGLVKKCMGFTVTLNQARGS 120
Db 60 LDQPPKADEDGTPKPVSFYTKVETCPRTTQSPEDCDFPKENGRVKQCVGTVTLQIKDP 119
QY 121 FDISCDK 127
Db 120 LDITCNE 126

RESULT 14
A53895
protegrin 3 precursor - pig
N;Alternate names: neutrophil peptide 2
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 01-Dec-1995 #sequence revision 01-Dec-1995 #text_change 09-Jul-2004
C;Accession: S66285; A53895; S34587; S36821; S57608
R;Zhao, C.; Ganz, T.; Lehrer, R.I.
FEBS Lett. 368, 197-202, 1995
A;Title: The structure of porcine protegrin genes.
A;Reference number: S66283; MUID:95354835; PMID:7628604
A;Accession: S66285
A;Molecule type: DNA
A;Residues: 1-149 <ZH3>
A;Cross-references: UNIPROT:P32196; UNIPARC:UPI0000131777; EMBL:X84095; NID:9887644; PID
R;Zhao, C.; Liu, L.; Lehrer, R.I.
FEBS Lett. 346, 285-288, 1994
A;Title: Identification of a new member of the protegrin family by cDNA cloning.
A;Reference number: S45712; MUID:94283613; PMID:8013647
A;Accession: A53895
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-149 <ZHA>
A;Cross-references: UNIPARC:UPI0000131777; GB:X83267; NID:G603037; PIDN:CAA58240.1; PID:
R;Kokryakov, V.N.; Harwig, S.S.L.; Panyutich, E.A.; Shevchenko, A.A.; Alekhina, G.M.; Sh
FEBS Lett. 327, 231-236, 1993
A;Title: Protegrins: leukocyte antimicrobial peptides that combine features of corticost

A;Reference number: S34585; MUID:93327946; PMID:8335113
A;Accession: S34587
A;Molecule type: protein
A;Residues: 131-148 <KOK>
A;Cross-references: UNIPARC:UPI0000143110
R;Mirgorodskaya, O.A.; Shevchenko, A.A.; Abdalla, K.O.M.A.; Chernushevich, I.V.; Egorov, F.B.S. Lett. 330, 339-342, 1993
A;Title: Primary structure of three cationic peptides from porcine neutrophils. Sequence
A;Reference number: S36820; MUID:93387466; PMID:8375505
A;Accession: S36821
A;Molecule type: protein
A;Residues: 131-148 <MIR>
A;Cross-references: UNIPARC:UPI0000143110
C;Genetics:
A;Gene: NPG3
A;Introns: 66/3; 102/3; 126/3
C;Superfamily: cathelin; cystatin homology
C;Keywords: amidated carboxyl end; antibacterial; neutrophil
F;1-29/Domain: signal sequence #status predicted <SIG>
F;22-129/Domain: cystatin homology <CYS>
F;30-130/Domain: propeptide #status predicted <PRO>
F;131-148/Product: proteogrin 3 #status experimental <MAT>
F;148/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gl

Query Match 47.6%; Score 418.5; DB 2; Length 149;
Best Local Similarity 65.4%; Pred. No. 9.5e-33;
Matches 83; Conservative 19; Mismatches 24; Indels 1; Gaps 1;
Qy 1 MKTQRDGHSLGRWSLVLLGLVMPPLAIIAQVLSYKEAVLRAIDGINORSSDANLYRLLD 60
Db 1 METQRASLCLGRWSLWLLALLVVPESA-SQAQALSYREAVLRAVDRLNEQSSEANLYRLLE 59
Qy 61 LDPRTMDGDDPTPKPVSVFTVKETVCPRTTQSPEDCDPKDGLVKRCMGTTVLNQARGS 120
Db 60 LDQPPKADEDGTPPKPVSVFTVKETVCPRTTQSPEDCDPKDGLVKRCMGTTVLNQARGS 119
Qy 121 FDISCDK 127
Db 120 LDITCNE 126
Qy 121 FDISCDK 127
Db 120 LDITCNE 126

RESULT 15
S57607
protegrin 1 precursor - pig
N;Alternate names: neutrophil peptide 1
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S56284; S45712; S36820; S34585; S57607
R;Zhao, C.; Ganz, T.; Lehrer, R.I.
FEBS Lett. 368, 197-202, 1995
A;Title: The structure of porcine proteogrin genes.
A;Reference number: S56283; MUID:95354835; PMID:7628604
A;Accession: S56284
A;Molecule type: DNA
A;Residues: 1-149 <ZHA>
A;Cross-references: UNIPROT:P32194; UNIPARC:UPI0000131775; EMBL:X84094; NID:g887642; PID
R;Zhao, C.; Liu, L.; Lehrer, R.I.
FEBS Lett. 346, 285-288, 1994
A;Title: Identification of a new member of the proteogrin family by cDNA cloning.
A;Reference number: S45712; MUID:94283613; PMID:8013647
A;Accession: S45712
A;Molecule type: mRNA
A;Residues: 1-149 <ZH2>
A;Cross-references: UNIPARC:UPI0000131775; GB:X79868; NID:g603035; PIDN:CAA56251.1; PID:
R;Mirgorodskaya, O.A.; Shevchenko, A.A.; Abdalla, K.O.M.A.; Chernushevich, I.V.; Egorov, F.B.S. Lett. 330, 339-342, 1993
A;Title: Primary structure of three cationic peptides from porcine neutrophils. Sequence
A;Reference number: S36820; MUID:93387466; PMID:8375505
A;Accession: S36820
A;Molecule type: protein
A;Residues: 131-148 <MIR>
A;Cross-references: UNIPARC:UPI0000034C2E
R;Kokryakov, V.N.; Harwig, S.S.L.; Panyutich, E.A.; Shevchenko, A.A.; Aleshina, G.M.; SH

FEBS Lett. 327, 231-236, 1993
A;Title: Protegrins: leukocyte antimicrobial peptides that combine features of corticost
A;Reference number: S34585; MUID:93327946; PMID:8335113
A;Accession: S34585
A;Molecule type: protein
A;Residues: 131-148 <KOK>
A;Cross-references: UNIPARC:UPI0000034C2E
C;Genetics:
A;Gene: NPG1
A;Introns: 66/3; 102/3; 126/3
C;Superfamily: cathelin; cystatin homology
C;Keywords: amidated carboxyl end; antibacterial; neutrophil
F;1-29/Domain: signal sequence #status predicted <SIG>
F;22-129/Domain: cystatin homology <CYS>
F;30-130/Domain: propeptide #status predicted <PRO>
F;131-148/Product: proteogrin 1 #status experimental <MAT>
F;148/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gl

Query Match 47.6%; Score 418.5; DB 2; Length 149;
Best Local Similarity 65.4%; Pred. No. 9.5e-33;
Matches 83; Conservative 19; Mismatches 24; Indels 1; Gaps 1;
Qy 1 MKTQRDGHSLGRWSLVLLGLVMPPLAIIAQVLSYKEAVLRAIDGINORSSDANLYRLLD 60
Db 1 METQRASLCLGRWSLWLLALLVVPESA-SQAQALSYREAVLRAVDRLNEQSSEANLYRLLE 59
Qy 61 LDPRTMDGDDPTPKPVSVFTVKETVCPRTTQSPEDCDPKDGLVKRCMGTTVLNQARGS 120
Db 60 LDQPPKADEDGTPPKPVSVFTVKETVCPRTTQSPEDCDPKDGLVKRCMGTTVLNQARGS 119
Qy 121 FDISCDK 127
Db 120 LDITCNE 126

Search completed: January 12, 2006, 21:51:07
Job time : 16.0554 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 12, 2006, 21:42:24 ; Search time 82.8044 Seconds
(without alignments)
1448.471 Million cell updates/sec

Title: US-10-815-562-2

Perfect score: 879
Sequence: 1 MKTQDGHSLGRWSLVLLLL.....KRIVQIKDFLRLVPTRES 170

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------------|--------------------|
| 1 | 879 | 100.0 | 170 | FAL39_HUMAN | P49913 homo sapien |
| 2 | 879 | 100.0 | 170 | FAL39_MACMU | Q71en9 macaca mula |
| 3 | 759 | 86.3 | 170 | Q9GLV5_MACMU | Q9GLV5 macaca mula |
| 4 | 498.5 | 56.7 | 157 | O62841_HORSE | O62841 equus cabal |
| 5 | 486.5 | 55.3 | 172 | O6TN20_CANFA | O6tn20 canis famil |
| 6 | 468.5 | 53.3 | 171 | CAP18_RABIT | P25230 oryctolagus |
| 7 | 457.5 | 52.0 | 170 | O62842_HORSE | O62842 equus cabal |
| 8 | 454 | 51.6 | 165 | BNA34_BOVIN | P56425 bos taurus |
| 9 | 453.5 | 51.6 | 171 | Q71KM5_RAT | Q71km5 rattus norv |
| 10 | 451 | 51.3 | 156 | O62840_HORSE | O62840 equus cabal |
| 11 | 444.5 | 50.6 | 167 | PMP37_PIG | P49932 sus scrofa |
| 12 | 443.5 | 50.5 | 166 | PMP36_PIG | P49931 sus scrofa |
| 13 | 442.5 | 50.3 | 176 | BCTN5_CAPHI | P82018 capra hircu |
| 14 | 442.5 | 50.3 | 176 | Q4JFB9_CAPHI | Q4jfb9 capra hircu |
| 15 | 440 | 50.1 | 165 | P79360_SHEEP | P79360 ovis aries |
| 16 | 438.5 | 49.9 | 153 | PMP23_PIG | P49930 sus scrofa |
| 17 | 437.5 | 49.8 | 176 | BCTN5_SHEEP | P79362 ovis aries |
| 18 | 433.5 | 49.3 | 173 | CRAMP_MOUSE | P51437 mus musculu |
| 19 | 432.5 | 49.2 | 155 | BCTN1_SHEEP | P54230 ovis aries |
| 20 | 432 | 49.1 | 158 | BNA27_BOVIN | P54228 bos taurus |
| 21 | 432 | 49.1 | 159 | BNA28_BOVIN | P54229 bos taurus |
| 22 | 431 | 49.0 | 165 | P82017_CAPHI | P82017 capra hircu |
| 23 | 429.5 | 48.9 | 228 | PF12_PIG | P51525 sus scrofa |
| 24 | 427.5 | 48.6 | 155 | BCTN1_BOVIN | P22226 bos taurus |
| 25 | 427.5 | 48.6 | 172 | PR39_PIG | P80054 sus scrofa |
| 26 | 424.5 | 48.3 | 149 | PG5_PIG | P49934 sus scrofa |
| 27 | 418.5 | 47.6 | 147 | PG2_PIG | P32195 sus scrofa |
| 28 | 418.5 | 47.6 | 149 | PG1_PIG | P32194 sus scrofa |
| 29 | 418.5 | 47.6 | 149 | PG3_PIG | P32196 sus scrofa |
| 30 | 418.5 | 47.6 | 149 | PG4_PIG | P49933 sus scrofa |
| 31 | 416.5 | 47.4 | 190 | BCTN7_BOVIN | P19661 bos taurus |

| | | | | | | |
|----|-------|------|-----|---|--------------|--------------------|
| 32 | 413 | 47.0 | 158 | 2 | Q9XSQ8_CAPHI | Q9xsq8 capra hircu |
| 33 | 412 | 46.9 | 160 | 1 | SC51_SHEEP | P49928 ovis aries |
| 34 | 410.5 | 46.7 | 176 | 1 | BCTN5_BOVIN | P19660 bos taurus |
| 35 | 406.5 | 46.2 | 144 | 2 | Q683R8_BUBBU | Q683r8 bubalus bub |
| 36 | 405.5 | 46.1 | 144 | 1 | INDC_BOVIN | P33046 bos taurus |
| 37 | 400 | 45.5 | 160 | 1 | SC52_SHEEP | P49929 ovis aries |
| 38 | 387.5 | 44.1 | 212 | 1 | PF11_PIG | P51524 sus scrofa |
| 39 | 385.5 | 43.9 | 190 | 2 | Q9XSQ9_CAPHI | Q9xsq9 capra hircu |
| 40 | 380.5 | 43.3 | 164 | 2 | P79361_SHEEP | P79361 ovis aries |
| 41 | 374.5 | 42.6 | 190 | 1 | BCTN7_SHEEP | P50415 ovis aries |
| 42 | 369.5 | 42.0 | 224 | 2 | O19031_SHEEP | O19031 ovis aries |
| 43 | 360.5 | 41.0 | 182 | 2 | O19040_SHEEP | O19040 ovis aries |
| 44 | 325 | 37.0 | 178 | 2 | Q91X12_CAVPO | Q91x12 cavia porce |
| 45 | 322.5 | 36.7 | 109 | 2 | Q920X4_MUSSI | Q920x4 mus spicile |

ALIGNMENTS

| | | | | | |
|----------|--|-----------|------|---------|--|
| RESULT 1 | | | | | |
| ID | FAL39_HUMAN | STANDARD; | PRT; | 170 AA. | |
| AC | P49913; | | | | |
| DT | 01-OCT-1996 (Rel. 34, Created) | | | | |
| DT | 01-OCT-1996 (Rel. 34, Last sequence update) | | | | |
| DT | 13-SEP-2005 (Rel. 48, Last annotation update) | | | | |
| DE | Antibacterial protein FALL-39 precursor (FALL-39 peptide antibiotic) | | | | |
| DE | (Cationic antimicrobial protein CAP-18) (hCAP-18) [Contains: | | | | |
| DE | Antibacterial protein LL-37]. | | | | |
| GN | Name=CAMP; Synonyms=CAP18, FALL39; | | | | |
| OS | Homo sapiens (Human). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | |
| OC | Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; | | | | |
| OC | Homo. | | | | |
| OX | NCBI_TaxID=9606; | | | | |
| RN | [1] | | | | |
| RP | NUCLEOTIDE SEQUENCE [MRNA], AND SYNTHESIS OF 132-170. | | | | |
| RC | TISSUE=Bone marrow; | | | | |
| RX | MEDLINE=95116523; PubMed=7529412; | | | | |
| RA | Agerberth B., Gunne H., Odeberg J., Kogner P., Roman H.G., | | | | |
| RA | Gudmundsson G.H.; | | | | |
| RT | "FALL-39, a putative human peptide antibiotic, is cysteine-free and | | | | |
| RT | expressed in bone marrow and testis."; | | | | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 92:195-199(1995). | | | | |
| [2] | | | | | |
| RP | NUCLEOTIDE SEQUENCE [MRNA], AND PROTEIN SEQUENCE OF 42-68 AND 83-100. | | | | |
| RC | TISSUE=Bone marrow; | | | | |
| RN | MEDLINE=95339969; PubMed=7615076; DOI=10.1016/0014-5793(95)00634-L; | | | | |
| EX | Cowland J.B., Johnsen A.H., Borregaard N.; | | | | |
| RA | "hCAP-18, a cathelin/pro-bactenecin-like protein of human neutrophil | | | | |
| RT | specific granules."; | | | | |
| RL | FEBS Lett. 368:173-176(1995). | | | | |
| [3] | | | | | |
| RP | NUCLEOTIDE SEQUENCE [MRNA]. | | | | |
| RC | TISSUE=Bone marrow; | | | | |
| RX | MEDLINE=95197251; PubMed=7890387; | | | | |
| RA | Larrick J.W., Hirata M., Balint R.F., Lee J., Zhong J., Wright S.C.; | | | | |
| RT | "Human CAP18: a novel antimicrobial lipopolysaccharide-binding | | | | |
| RT | protein."; | | | | |
| RL | Infect. Immun. 63:1291-1297(1995). | | | | |
| [4] | | | | | |
| RP | NUCLEOTIDE SEQUENCE [GENOMIC DNA]. | | | | |
| RN | MEDLINE=97102716; PubMed=8946956; DOI=10.1016/S0014-5793(96)01199-4; | | | | |
| RX | Larrick J.W., Lee J., Ma S., Li X., Francke U., Wright S.C.; | | | | |
| RA | Ballint R.F.; | | | | |
| RT | "Structural, functional analysis and localization of the human CAP18 | | | | |
| RT | gene."; | | | | |
| RL | FEBS Lett. 398:74-80(1996). | | | | |
| [5] | | | | | |
| RP | NUCLEOTIDE SEQUENCE [GENOMIC DNA]. | | | | |
| RN | PubMed=8681941; | | | | |
| RX | Gudmundsson G.H., Agerberth B., Odeberg J., Bergman T., Olsson B., | | | | |
| RA | Salcedo R.; | | | | |

"The human gene FALL39 and processing of the cathelin precursor to the antibacterial peptide LL-37 in granulocytes.",
Eur. J. Biochem. 238:325-332(1996).
[6]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Epithelium;
RA Gao Y., Huang Y.F., Xia X.Y.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
[7]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Testis;
RA Wu N., Miao S.Y., Zhang X.D., Qiao Y., Liang G., Wang L.F.;
RL "A new spermatogenesis-related gene."
[8]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA Halleck A., Ebert L., Moundinya M., Schick M., Eisenstein S.,
RA Neubert P., Ketrang K., Schatzen R., Shen B., Henze S., Mar W.,
RA Kohn B., Zuo D., Hu Y., LaBaer J.;
RL "Cloning of human full open reading frames in Gateway(TM) system entry vector (pDONR201)."
[9]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marais K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RL "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
[10]
RP Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Binds to bacterial lipopolysaccharides (LPS), has antibacterial activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed in bone marrow and testis and neutrophils.
CC -!- PTM: The N-terminus is blocked.
CC -!- SIMILARITY: Belongs to the cathelicidin family.

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DR EMBL; Z38026; CRA86115.1; -; mRNA.
DR EMBL; X89658; CAA61805.1; -; mRNA.
DR EMBL; U19570; AAG74084.1; -; mRNA.
DR EMBL; U48795; AAC02634.1; -; Genomic DNA.
DR EMBL; X96735; -; NOT_ANNOTATED_CDS; Genomic DNA.
DR EMBL; AY162210; AAN78318.1; -; mRNA.
DR EMBL; AY251531; AAP20054.1; -; mRNA.
DR EMBL; CR457083; CAG33364.1; -; mRNA.
DR EMBL; CR541961; CAG46759.1; -; mRNA.
DR EMBL; BC055089; AAH55089.1; -; mRNA.
DR PIR; I38932; I38932.
DR PIR; S74248; S74248.
DR HSGP; P32196; 1KWI.
DR Ensembl; ENSG00000164047; Homo sapiens.

DR HGNC; HGNC:1472; CAMP.
DR MIM; 600474; -.
DR GO; GO:0042742; P:defense response to bacteria; TAS.
DR InterPro; IPR001894; Cathelicidin.
DR PANTHER; PTHR10206; Cathelicidin; 1.
DR Pfam; PF00666; Cathelicidins; 1.
DR ProDom; PD001838; Cathelicidin; 1.
DR PROSITE; PS00946; CATHELICIDINS_1; 1.
DR PROSITE; PS00947; CATHELICIDINS_2; 1.
KW Antibiotic; Antimicrobial; Direct protein sequencing;
KW Pyrrolidone carboxylic acid; Signal.
FT SIGNAL 1 30 Potential.
FT PROPEP 31 131
FT CHAIN 132 170 Antibacterial protein FALL-39.
FT CHAIN 134 170 Antibacterial protein LL-37.
FT MOD_RES 31 31 Pyrrolidone carboxylic acid (By similarity).
FT DISULFID 86 97 By similarity.
FT DISULFID 108 125 By similarity.
FT CONFLICT 6 D -> N (in Ref. 1, 6, 7 and 8; CAG46759).
SQ SEQUENCE 170 AA; 19301 MW; 055B07DCA95A7D16 CRC64;
Query Match 100.0%; Score 879; DB 1; Length 170;
Best Local Similarity 100.0%; Pred. No. 6.9e-76;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKTQDGHSLGRWSLVLLLLGLVNPFLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
DB 1 MKTQDGHSLGRWSLVLLLLGLVNPFLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
QY 61 LDPRTMDGDDPTPKPVSTVKTVCPTTQSPEDCDPKDGLVKRCMGVTTLNQARGS 120
DB 61 LDPRTMDGDDPTPKPVSTVKTVCPTTQSPEDCDPKDGLVKRCMGVTTLNQARGS 120
QY 121 FDISCDKDKRFPALLGDFFRKSKKIGKEPKRIQVRIKDFLRNLVPRTES 170
DB 121 FDISCDKDKRFPALLGDFFRKSKKIGKEPKRIQVRIKDFLRNLVPRTES 170
RESULT 2
FALL39_MACMU STANDARD; PRT; 170 AA.
ID FALL39_MACMU
AC Q71SN9;
DT 10-MAY-2005 (Rel. 47, Created)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Antibacterial protein FALL-39 precursor (FALL-39 peptide antibiotic)
DE (Cationic antimicrobial protein CAP-18) (rHCAP-18) [Contains:
DE Antibacterial protein LL-37 (rHL-37)].
GN Name=CAMP; Synonyms=CAP18, FALL39;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
[1]
RP NUCLEOTIDE SEQUENCE [MRNA], AND TISSUE SPECIFICITY.
RA MEDLINE=21137962; PubMed=11239224; DOI=10.1128/CDLI.8.2.370-375.2001;
RA Bais R., Lang C., Weiner D.J., Vogelmeier C., Welsch U., Wilson J.M.;
RT "Rhesus monkey (Macaca mulatta) mucosal antimicrobial peptides are
RT close homologues of human molecules."
RL Clin. Diagn. Lab. Immunol. 8:370-375(2001).
CC -!- FUNCTION: Binds to bacterial lipopolysaccharides (LPS), has antibacterial activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed in epithelia of various organs. Most abundant peptide levels are found in organs lining outer or inner body surfaces, such as organs of the respiratory or gastrointestinal tract.
CC -!- SIMILARITY: Belongs to the cathelicidin family.

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 CC use as long as its content is in no way modified and this statement is not
 CC removed.

DR EMBL; AF288284; AAG40802.1; -; mRNA.
 DR InterPro; IPR001894; Cathelicidin.
 DR PANTHER; PTHR10206; Cathelicidin; 1.
 DR Pfam; PF00666; Cathelicidins; 1.
 DR ProDom; PD001838; Cathelicidins; 1.
 DR PROSITE; PS00946; CATHELICIDINS_2; 1.
 DR PROSITE; PS00947; CATHELICIDINS_1; 1.
 KW Antibiotic; Antimicrobial; Pyrrolidone carboxylic acid; Signal.
 FT SIGNAL 1 30 Potential.
 FT PROPEP 31 131 Potential.
 FT CHAIN 132 170 Antibacterial protein FALL-39.
 FT CHAIN 134 170 Antibacterial protein LL-37.
 FT MOD_RES 31 31 Pyrrolidone carboxylic acid (By
 FT similarity).
 SQ SEQUENCE 170 AA; 19301 MW; 055B07DCA95A7D16 CRC64;

Query Match 100.0%; Score 879; DB 1; Length 170;
 Best Local Similarity 100.0%; Pred. No. 6.9e-76;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKTQDGHSLGRWSLVLLLLGLVNPPLAIIAQLVSYKEAVLRADGINQRSSDANLYRLLD 60
 Db 1 MKTQDGHSLGRWSLVLLLLGLVNPPLAIIAQLVSYKEAVLRADGINQRSSDANLYRLLD 60
 Qy 61 LDRPRTMDGDDPTPKPVSTVKETVCPRTTQQSPEDCDPKDGLVKRCMGVTTLNQARGS 120
 Db 61 LDRPRTMDGDDPTPKPVSTVKETVCPRTTQQSPEDCDPKDGLVKRCMGVTTLNQARGS 120
 Qy 121 FDISCDKNRKFALLGDFPRKSKKIGKFKRIVQRIKDFLRNLVPRTES 170
 Db 121 FDISCDKNRKFALLGDFPRKSKKIGKFKRIVQRIKDFLRNLVPRTES 170

RESULT 3

Q9GLV5 MACMU
 ID O9GLV5 MACMU PRELIMINARY; PRT; 170 AA.
 AC O9GLV5
 DT 01-MAR-2001 (TRENBLrel. 16, Created)
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Cathelin.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopithecoidea; Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Bone marrow;
 RX MEDLINE=21441139; PubMed=11557457;
 RX DOI=10.1128/JAC.45.10.2695-2702.2001;
 RA Zhao C., Nguyen T., Boo L.M., Hong T., Espiritu C., Orlov D., Wang W.,
 RA Waring A., Lehrer R.I.;
 RT "RL-37, an alpha-helical antimicrobial peptide of the rhesus monkey."
 RL Antimicrob. Agents Chemother. 45:2695-2702(2001).
 DR EMBL; AF181954; AAG09440.1; -; mRNA.
 DR HSSP; P32196; 1KWI.
 DR GO; GO:0005576; C:extracellular region; IEA.
 DR GO; GO:0006952; P:response to pest, pathogen or parasite; IEA.
 DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
 DR InterPro; IPR001894; Cathelicidin.
 DR Pfam; PF00666; Cathelicidins; 1.
 DR ProDom; PD001838; Cathelicidin; 1.
 DR PROSITE; PS00946; CATHELICIDINS_1; 1.
 DR PROSITE; PS00947; CATHELICIDINS_2; 1.
 SQ SEQUENCE 170 AA; 18861 MW; 355AB3BF510DBB83 CRC64;

Query Match 86.3%; Score 759; DB 2; Length 170;
 Best Local Similarity 86.5%; Pred. No. 2.1e-64;

Matches 147; Conservative 11; Mismatches 12; Indels 0; Gaps 0;
 Qy 1 MKTQDGHSLGRWSLVLLLLGLVNPPLAIIAQLVSYKEAVLRADGINQRSSDANLYRLLD 60
 Db 1 MKTQDGHSLGRWSLVLLLLGLVNPPLAIIAQLVSYKEAVLRADGINQRSSDANLYRLLD 60
 Qy 61 LDRPRTMDGDDPTPKPVSTVKETVCPRTTQQSPEDCDPKDGLVKRCMGVTTLNQARGS 120
 Db 61 LDRPRTMDGDDPTPKPVSTVKETVCPRTTQQSPEDCDPKDGLVKRCMGVTTLNQARGS 120
 Qy 121 FDISCDKNRKFALLGDFPRKSKKIGKFKRIVQRIKDFLRNLVPRTES 170
 Db 121 FDISCDKNRKFALLGDFPRKSKKIGKFKRIVQRIKDFLRNLVPRTES 170

RESULT 4

O62841 HORSE
 ID O62841 HORSE PRELIMINARY; PRT; 157 AA.
 AC O62841
 DT 01-AUG-1998 (TRENBLrel. 07, Created)
 DT 01-AUG-1998 (TRENBLrel. 07, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Myeloid cathelicidin 2 precursor.
 GN Name=eCATH-2;
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Bone marrow;
 RX MEDLINE=99402973; PubMed=10471829; DOI=10.1016/S0014-5793(99)01097-2;
 RA Scocchi M., Bontempo D., Boscolo S., Tomasinsig L., Giulotto E.,
 RA Zanetti M.;
 RT "Novel cathelicidins in horse leukocytes."
 RL FEBS Lett. 457:459-464(1999).
 DR EMBL; AJ224928; CAAL2227.1; -; mRNA.
 DR HSSP; P32196; 1KWI.
 DR SMR; O62841; 30-130.
 DR GO; GO:0005576; C:extracellular region; IEA.
 DR GO; GO:0006952; P:defense response; IEA.
 DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
 DR InterPro; IPR001894; Cathelicidin.
 DR Pfam; PF00666; Cathelicidins; 1.
 DR ProDom; PD001838; Cathelicidin; 1.
 DR PROSITE; PS00946; CATHELICIDINS_1; 1.
 DR PROSITE; PS00947; CATHELICIDINS_2; 1.
 KW Signal.
 FT SIGNAL 1 29 Potential.
 FT CHAIN 30 157 myeloid cathelicidin 2.
 SQ SEQUENCE 157 AA; 18153 MW; 1424C493D2B307CC CRC64;

Query Match 56.7%; Score 498.5; DB 2; Length 157;
 Best Local Similarity 76.4%; Pred. No. 1.7e-39;
 Matches 97; Conservative 13; Mismatches 16; Indels 1; Gaps 1;

Qy 1 MKTQDGHSLGRWSLVLLLLGLVNPPLAIIAQLVSYKEAVLRADGINQRSSDANLYRLLD 60
 Db 1 METQDSCSLGRWSLVLLLLGLVNPPLAIIAQLVSYKEAVLRADGINQRSSDANLYRLLE 59
 Qy 61 LDRPRTMDGDDPTPKPVSTVKETVCPRTTQQSPEDCDPKDGLVKRCMGVTTLNQARGS 120
 Db 60 LDPLPKEDDDPTPKPVSTVKETVCPRTTQQSPEDCDPKDGLVKRCMGVTTLNQARGS 119
 Qy 121 FDISCDK 127
 Db 120 FDISCDK 126

RESULT 5

O6TN20 CANFA
 ID O6TN20 CANFA PRELIMINARY; PRT; 172 AA.
 AC O6TN20;

DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Cathelicidin.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sang Y., Rune K., Melgarejo T., Blecha F.;
RL Submitted (SBB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY392089; AAR26245.1; -; mRNA.
DR Ensembl; ENSCAFG0000012896; Canis familiaris.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009633; P:response to pest, pathogen or parasite; IEA.
DR InterPro; IPR001894; Cathelicidin.
DR Pfam; PF00666; Cathelicidins; 1.
DR ProDom; PD001838; Cathelicidin; 1.
SQ SEQUENCE 172 AA; 19437 MW; 549EAC408DEB7A63 CRC64;
Query Match 55.3%; Score 486.5; DB 2; Length 172;
Best Local Similarity 57.9%; Pred. No. 2.7e-38;
Matches 99; Conservative 27; Mismatches 42; Indels 3; Gaps 2;
Qy 1 MKTQDGHSLGRWSLVLLLLGLVMPALIAIQVLSYKEAVLRADGINQRSDANLYRLLD 60
Db 1 METQKDSPLSGRLSLLLLGLLVITPA-ASRALSYREAVLRVNGFNQRSEENLYRLIQ 59
Qy 61 LDPRTWDGDDPTPKPVSTFKVETVCPRTTQSPEDCFKDGIVKRCMGVTTLNQARGS 120
Db 60 LNSQPKGEDNIPFAPVSTFKVETVCPRTTQSPEDCFKDGIVKRCMGVTTLNQARGS 119
Qy 121 FDISCDK--DNKRFPALLGDFFRKSKKIGKFKRIVQRKIDFLRLNLPVPRTE 169
Db 120 FDLNCDSILQVKKIDRLAKELITGQKIGEKIRRIGQRIKDFKFNQLQPRE 170
RESULT 6
ID CAP18 RABIT STANDARD; PRT; 171 AA.
AC P25230;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Antimicrobial protein CAP18 precursor (18 kDa lipopolysaccharide-
binding protein) (18 kDa cationic protein) (CAP18-A) [Contains:
Antimicrobial protein CAP7].
GN Name=CAP18;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 135-159.
RC TISSUE=Bone marrow;
RA Larick J.W., Morgan J.G., Palings I., Hirata M., Yen M.H.;
RX MEDLINE=91354246; PubMed=1883348;
RT "Complementary DNA sequence of rabbit CAP18 -- a unique
lipopolysaccharide binding protein.";
RL Biochem. Biophys. Res. Commun. 179:170-175(1991).
RN [2]
RP PROTEIN SEQUENCE OF 135-159, AND CHARACTERIZATION.
RX MEDLINE=94178952; PubMed=8132348;
RA Hirata M., Shimomura Y., Yoshida M., Morgan J.G., Palings I.,
RA Wilson D., Yen M.H., Wright S.C., Larick J.W.;
RT "Characterization of a rabbit cationic protein (CAP18) with
lipopolysaccharide-inhibitory activity.";
RL Infect. Immun. 62:1421-1426(1994).
RN [3]

RP PROTEIN SEQUENCE OF 135-154, AND CHARACTERIZATION.
RX MEDLINE=94075827; PubMed=8254193;
RA Larick J.W., Hirata M., Zheng H., Zhong J., Bolin D.,
RA Cavallion J.-M., Warren H.S., Wright S.C.;
RT "A novel granulocyte-derived peptide with lipopolysaccharide-
neutralizing activity.";
RL J. Immunol. 152:231-240(1994).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=94148064; PubMed=8313956; DOI=10.1016/0014-5793(94)80395-1;
RA Tossi A., Scocchi M., Skerlavaj B., Gennaro R.;
RT "Identification and characterization of a primary antibacterial domain
in CAP18, a lipopolysaccharide binding protein from rabbit
leukocytes.";
RL FEBS Lett. 339:108-112(1994).
RN [5]
RP STRUCTURE BY NMR OF 135-166.
RX MEDLINE=95377455; PubMed=7649303; DOI=10.1016/0014-5793(95)00792-8;
RA Chen C., Brock R., Luh F., Chou P.-J., Larick J.W., Huang R.-P.,
RA Huang T.-H.;
RT "The solution structure of the active domain of CAP18 -- a
lipopolysaccharide binding protein from rabbit leukocytes.";
RL FEBS Lett. 370:46-52(1995).
CC -!- FUNCTION: CAP18 binds to the lipid moiety of bacterial
lipopolysaccharides (LPS), a glycolipid present in the outer
membrane of all Gram-negative bacteria. Has antibiotic activity.
CC -!- TISSUE SPECIFICITY: Neutrophils.
CC -!- SIMILARITY: Belongs to the cathelicidin family.
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removed.
DR PDB; 1LYP; NMR; @=135-166.
DR InterPro; IPR001894; Cathelicidin.
DR PANTHER; PTHR10206; Cathelicidin; 1.
DR Pfam; PF00666; Cathelicidins; 1.
DR ProDom; PD001838; Cathelicidin; 1.
DR PROSITE; PS00946; CATHELICIDINS 1; 1.
DR PROSITE; PS00947; CATHELICIDINS 2; 1.
KW 3D-structure; Antibiotic; Antimicrobial; Direct protein sequencing;
KW Pyrrolidone carboxylic acid; Signal.
FT SIGNAL 1 29 Potential.
FT CHAIN 30 171 Antimicrobial protein CAP18.
FT CHAIN 135 171 Antimicrobial protein CAP7.
FT MOD_RES 30 30 Pyrrolidone carboxylic acid (By
similarity).
FT DISULFID 85 96 By similarity.
FT DISULFID 107 124 By similarity.
FT VARIANT 157 157 K -> D.
SQ SEQUENCE 171 AA; 19805 MW; D7BF2103BCFB13C4 CRC64;
Query Match 53.3%; Score 468.5; DB 1; Length 171;
Best Local Similarity 57.3%; Pred. No. 1.4e-36;
Matches 98; Conservative 27; Mismatches 43; Indels 3; Gaps 2;
Qy 1 MKTQDGHSLGRWSLVLLLLGLVMPALIAIQVLSYKEAVLRADGINQRSDANLYRLLD 60
Db 1 METHKHGSPSLAWSLLLLGLLLMPPA-IAQDLTYREAVLRADVAFNQSQSEANLYRLLS 59
Qy 61 LDPRTWDGDDPTPKPVSTFKVETVCPRTTQSPEDCFKDGIVKRCMGVTTLNQARGS 120
Db 60 MDPQOLEDAKPYTPQPVSTFKVETVCPRTTQSPEDCFKDGIVKRCMGVTTLNQARGS 119
Qy 121 FDISCDK--DNKRFPALLGDFFRKSKKIGKFKRIVQRKIDFLRLNLPVPRTE 169
Db 120 FDIKCNRAQSPSPBTGLRKLRKLRFNKIKELKKIKGKIQGVFKLAPRTD 170
RESULT 7

```

RL  FBBS Lett. 417:311-315 (1997).
CC -1- FUNCTION: Exerts a potent antimicrobial activity.
CC -1- TISSUE SPECIFICITY: Expressed in bone marrow myeloid cells, spleen
CC and testis.
CC -1- SIMILARITY: Belongs to the cathelicidin family.
-----
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
DR EMBL; Y12729; CAA73261.1; -; Genomic_DNA.
DR EMBL; Y12728; CAA73261.1; JOINED; Genomic_DNA.
DR HSSP; P32196; 1KW1.
DR SMR; P56425; 30-129.
DR InterPro; IPR001894; Cathelicidin.
DR PANTHER; PTHR10206; Cathelicidin; 1.
DR Pfam; PF00666; Cathelicidins; 1.
DR ProDom; PD001838; Cathelicidin; 1.
DR PROSITE; PS00946; CATHELICIDINS 1; 1.
DR PROSITE; PS00947; CATHELICIDINS 2; 1.
DR Amidation; Antibiotic; Antimicrobial; Pyrrolidone carboxylic acid;
KW Signal.
KW FT SIGNAL 1 29 Potential.
FT FT PROPEP 30 130 Potential.
FT FT PEPTIDE 131 165 Antibacterial peptide BMAP-34.
FT FT MOD_RES 30 30 Pyrrolidone carboxylic acid.
FT FT MOD_RES 165 165 Glycine amide (Potential).
FT FT DISULFID 86 97 By similarity.
FT FT DISULFID 108 125 By similarity.
FT SQ SEQUENCE 165 AA; 18848 MW; 21F14A0A68C6BF0 CRC64;
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Query Match 51.6%; Score 454; DB 1; Length 165;
Best Local Similarity 60.0%; Pred.No.3.3e-35;
Matches 99; Conservative 21; Mismatches 41; Indels 4; Gaps 3;
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QY 1 MKTQRDGHSLGRWSLVLLLLGLVPLAIIAQVLSYKEAVLRAIDGINRSSDANLYRLLD 60
Db 1 METQRASFSLGRSSLLWLLLLGLVWPSA-SAQDLSYREAVLRAVDQFNERSSEANLYRLLE 59
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QY 61 LDRPTMDGD-PDTPEVSEFTVKETCPRTTQSPEDCDFKKGDLVKRCNGTITLQAQRG 119
Db 60 LDPPEQDVEHPGKAPVSEFTVKETCPRTTQPPQPCDFKENGVLKQCQGTVTYRWIRG 119
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QY 120 SFDISCDKNKR--PALIGDFPRKSEKIGKSPRIVQRIKDFLR 162
Db 120 DFDITCNNTQSAGLFRRLRDSIRRGQOKILEKARRIGERIKDIFR 164
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RESULT 9
Q71KM5 RAT PRELIMINARY; PRT; 171 AA.
ID Q71KM5 RAT PRELIMINARY;
AC Q71KM5;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE CRAMP (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley;
RA Termen S., Tollin M., Olason B., Svenberg T., Agerberth B.,
RA Gudmundsson G.H.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; A9484553; AAQ05977.1; -; mRNA.
DR GO; GO:000576; C:extracellular region; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009613; P:response to pest pathogen or parasite; IEA.

```

```
DR InterPro; IPR001894; Cathelicidin.
DR Pfam; PF00666; Cathelicidins; 1.
DR ProDom; PD001838; Cathelicidin; 1.
DR PROSITE; PS00946; CATHELICIDINS_1; 1.
DR PROSITE; PS00947; CATHELICIDINS_2; 1.
FT NON_TER 1
SQ SEQUENCE 171 AA; 19320 MW; 788F3DA9DF10E839 CRC64;

Query Match 51.6%; Score 453.5; DB 2; Length 171;
Best Local Similarity 55.6%; Pred. No. 3.8e-35;
Matches 95; Conservative 21; Mismatches 48; Indels 7; Gaps 2;

Qy 5 RDGSLGRWSLVLLLLGLVMPALAIQAQLSYKEAVLRADIDGINORSSDANLYRLDLDP 64
Db 1 RDVPSLRWSLSLLLLGLGLPLT-VSQTLSTREAVLRVDVFNQSLDTNLYRLDLDS 59

Qy 65 PTMGDDPTPKVSFTVKETCPRTTQSPEDCFKKDGLVKRCMGVTTLNQAQSGFDS 124
Db 60 PQGDEDDPTPKYVFRVKETVCSKASQQLPEQCAFKEQGVVKQCMGTVTTLNRAAESFDS 119

Qy 125 CDKDN-----KRFALLGDFPRKSKKEKIGKFKRIVQRIKDFLRNLVPRTE 169
Db 120 CDAPGIDPRFKKISRLAGLLRKGGEKFGKLRKIGQIKDFFQKLAPEIE 170

RESULT 10
O62840 HORSE PRELIMINARY; PRT; 156 AA.
AC O62840;
DT 01-AUG-1998 (Tremblrel. 07, Created)
DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Myeloid cathelicidin 1 precursor.
GN Name=cath-1;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Bone marrow;
RX MEDLINE=99402973; PubMed=10471829; DOI=10.1016/S0014-5793(99)01097-2;
RA Scocchi M., Bontempo D., Boscolo S., Tomasinsig L., Giulotto E.,
RA Zanetti M.;
RT "Novel cathelicidins in horse leukocytes.";
RL FEBS Lett. 457:459-464(1999).
DR EMBL; AJ224927; CAAL12226.1; -; mRNA.
DR HSSP; P32196; 1KWI.
DR SMR; O62840; 30-130.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
DR InterPro; IPR001894; Cathelicidin.
DR Pfam; PF00666; Cathelicidins; 1.
DR ProDom; PD001838; Cathelicidin; 1.
DR PROSITE; PS00946; CATHELICIDINS_1; 1.
DR PROSITE; PS00947; CATHELICIDINS_2; 1.
KW Signal.
FT SIGNAL 1 29 Potential.
FT CHAIN 30 156 Potential.
SQ SEQUENCE 156 AA; 17647 MW; BB8EA5D150288FFD CRC64;

Query Match 51.3%; Score 451; DB 2; Length 156;
Best Local Similarity 56.2%; Pred. No. 6e-35;
Matches 95; Conservative 20; Mismatches 32; Indels 22; Gaps 4;

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Db 1 METQRTCLGRWSLVLLLLGLGLVTPPA-TTQALSYKEAVLRADVGLNQRSSDENLYRL 59

Qy 61 LDPRPTMGDDPTPKPVSFTVKETVCPRTTQSPEDCFKKDGLVKRCMGVTTLNQAQSG 120
Db 60 LDPLPKGDKSDTPKPVSMVKETVCPRTTQSPEDCFKKDGLVKRCMGVTTLNQAQSG 119
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Qy 121 FDISCDKN--KRFALLGDFPRKSKKEKIGKFKRIVQRIKDFLRNLVPR 167
Db 120 FVSCGEPQVRKFG-----RLAKSFLR-----MILLPR 149

RESULT 11
PMP37 PIG STANDARD; PRT; 167 AA.
AC P49932;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Antibacterial peptide PMAP-37 precursor (Myeloid antibacterial peptide 37).
GN Name=PMAP37;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND SYNTHESIS OF 131-167.
RC TISSUE=Bone marrow;
RX MEDLINE=95255306; PubMed=7737198;
RA Tossi A., Scocchi M., Zanetti M., Storici P., Gennaro R.;
RT "PMAP-37, a novel antibacterial peptide from pig myeloid cells. cDNA cloning, chemical synthesis and activity.";
RL Eur. J. Biochem. 228:941-946(1995).
CC -!- FUNCTION: Exerts antimicrobial activity against both Gram-positive and negative bacteria with minimal inhibitory concentrations ranging over 1-4 micro molar. Its activity appears to be mediated by its ability to damage bacterial membranes.
CC -!- SIMILARITY: Belongs to the cathelicidin family.

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EMBL; L39641; AAA63447.1; -; mRNA.
PIR; S68967; S68967.
HSSP; P32196; 1KWI.
SMR; P49932; 30-130.
InterPro; IPR001894; Cathelicidin.
PANTHER; PTHR10206; Cathelicidins; 1.
Pfam; PF00666; Cathelicidins; 1.
ProDom; PD001838; Cathelicidin; 1.
PROSITE; PS00946; CATHELICIDINS_1; 1.
PROSITE; PS00947; CATHELICIDINS_2; 1.
KW Antibiotic; Antimicrobial; Pyrrolidone carboxylic acid; Signal.
FT SIGNAL 1 29 Potential.
FT PROPEP 30 130 Potential.
FT PEPTIDE 131 167 Pyrrolidone carboxylic acid (By similarity).
FT MOD_RES 30 30 By similarity.
FT DISULFID 85 96 By similarity.
FT DISULFID 107 124 By similarity.
SQ SEQUENCE 167 AA; 18927 MW; 20F2B95966432992 CRC64;

Query Match 50.6%; Score 444.5; DB 1; Length 167;
Best Local Similarity 57.1%; Pred. No. 2.7e-34;
Matches 92; Conservative 26; Mismatches 40; Indels 3; Gaps 2;

Qy 1 MKTQDGHSLGRWSLVLLLLGLVMPALAIQAQLSYKEAVLRADIDGINORSSDANLYRL 60
Db 1 METQRTCLGRWSLVLLLLGLVTPPA-TTQALSYKEAVLRADVGLNQRSSDENLYRL 59

Qy 61 LDPRPTMGDDPTPKPVSFTVKETVCPRTTQSPEDCFKKDGLVKRCMGVTTLNQAQSG 120
Db 60 LDOPPKADEDPGTPKPVSMVKETVCPRTTQSPEDCFKKDGLVKRCMGVTTLNQAQSG 119
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RN [1]

CC -I- FUNCTION: Exerts antimicrobial activity against both Gram-positive

22

22

DR PIR; S41731; S41731.

DR InterPro: IPR001894: Cathelicidin.

DR ProDom: PD001838; Cathellicidin: 1.

KW Antibiotic: Antimicrobial: Pyrrolidone carboxylic acid: signal.

| FT | PROPEP | 30 | 129 | Potential |
|----|--------|----|-----|-----------|
| | | | | |

| FT | MOD_KBS | 30 | 30 | 30 | pyridine carboxylic acid (by similarity) |
|----|---------|----|----|----|--|
| FT | | | | | |

| FT | DISCREF ID | 83 | 30 | By similarity. |
|----|-------------|-----|-----|----------------|
| FT | DISINT. STD | 107 | 124 | By similarity |

NO CONVENTS 100 HR; 1004 / NM; 74B5C03 / 03DA04B CAC04;

| Method | 50 | 10 | Microtubules | 20 | Indol | 3 | Days |
|-----------------|---------|----|--------------|----|-------|---|------|
| BEAC POSITIVITY | 61.34 | | | | | | |
| PREQ. NO. | 3.3E-34 | | | | | | |

1. **מטרה:** להבין את חשיבות התחזוקה השוטפת של מערכת המים.

1 METOPROLOL CITRATE TABLETS - 50 MG

Q: 21. What is the purpose of the study?

[illegible]

א. זמנים - 15 דקות

䷗

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rnp) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:
<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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OM protein - .protein search, using sw model

Run on: January 12, 2006, 21:45:19 ; Search time 26.3469 Seconds
(without alignments)
533.455 Million cell updates/sec

Title: US-10-815-562-2

Perfect score: 879

Sequence: 1 MKTQDGHSLGRWSLVLLLL.....KRIVQRIKDFLNLVPTRES 170

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgm2_6/ptodata/1/iaa/5 COMB.pep.*
2: /cgm2_6/ptodata/1/iaa/6 COMB.pep.*
3: /cgm2_6/ptodata/1/iaa/H COMB.pep.*
4: /cgm2_6/ptodata/1/iaa/PCTUS COMB.pep.*
5: /cgm2_6/ptodata/1/iaa/RE COMB.pep.*
6: /cgm2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-----------------------|--------------------|
| 1 | 879 | 100.0 | 170 | 1 US-08-313-681A-2 | Sequence 2, Appli |
| 2 | 879 | 100.0 | 170 | 2 US-09-322-911-2 | Sequence 2, Appli |
| 3 | 874 | 99.4 | 170 | 2 US-09-917-340-32 | Sequence 32, Appli |
| 4 | 761 | 86.6 | 152 | 2 US-09-513-999C-7862 | Sequence 7862, Ap |
| 5 | 465.5 | 53.0 | 171 | 1 US-08-313-681A-4 | Sequence 4, Appli |
| 6 | 465.5 | 53.0 | 171 | 2 US-09-322-911-4 | Sequence 4, Appli |
| 7 | 457.5 | 52.0 | 170 | 2 US-09-917-340-33 | Sequence 33, Appli |
| 8 | 451 | 51.3 | 156 | 2 US-09-917-340-35 | Sequence 35, Appli |
| 9 | 432 | 49.1 | 159 | 2 US-09-917-340-34 | Sequence 34, Appli |
| 10 | 427.5 | 48.6 | 155 | 2 US-09-917-340-29 | Sequence 29, Appli |
| 11 | 418.5 | 47.6 | 147 | 1 US-08-243-879A-38 | Sequence 38, Appli |
| 12 | 418.5 | 47.6 | 147 | 1 US-08-499-523-4 | Sequence 4, Appli |
| 13 | 418.5 | 47.6 | 147 | 2 US-09-128-345-4 | Sequence 4, Appli |
| 14 | 418.5 | 47.6 | 149 | 1 US-08-243-879A-36 | Sequence 36, Appli |
| 15 | 418.5 | 47.6 | 149 | 1 US-08-243-879A-40 | Sequence 40, Appli |
| 16 | 418.5 | 47.6 | 149 | 1 US-08-243-879A-42 | Sequence 42, Appli |
| 17 | 418.5 | 47.6 | 149 | 1 US-08-499-523-2 | Sequence 2, Appli |
| 18 | 418.5 | 47.6 | 149 | 1 US-08-499-523-6 | Sequence 6, Appli |
| 19 | 418.5 | 47.6 | 149 | 1 US-08-499-523-8 | Sequence 8, Appli |
| 20 | 418.5 | 47.6 | 149 | 1 US-08-499-523-10 | Sequence 10, Appli |
| 21 | 418.5 | 47.6 | 149 | 2 US-09-128-345-2 | Sequence 2, Appli |
| 22 | 418.5 | 47.6 | 149 | 2 US-09-128-345-6 | Sequence 6, Appli |
| 23 | 418.5 | 47.6 | 149 | 2 US-09-128-345-8 | Sequence 8, Appli |
| 24 | 418.5 | 47.6 | 149 | 2 US-09-128-345-10 | Sequence 10, Appli |
| 25 | 415.5 | 47.3 | 147 | 2 US-09-385-328-4 | Sequence 4, Appli |
| 26 | 415.5 | 47.3 | 149 | 2 US-09-385-328-2 | Sequence 2, Appli |
| 27 | 415.5 | 47.3 | 149 | 2 US-09-385-328-6 | Sequence 6, Appli |

28 415.5 47.3 149 2 US-09-385-328-8 Sequence 8, Appli
29 412 46.9 160 2 US-09-917-340-36 Sequence 36, Appli
30 410.5 46.7 176 2 US-09-917-340-28 Sequence 28, Appli
31 333 37.9 78 2 US-09-513-999C-4349 Sequence 4349, Ap
32 325 37.0 96 1 US-08-313-681A-5 Sequence 5, Appli
33 325 37.0 96 2 US-09-322-911-5 Sequence 5, Appli
34 314 35.7 59 2 US-09-621-976-7180 Sequence 7180, Ap
35 203.5 23.2 66 2 US-09-385-328-17 Sequence 17, Appli
36 197.5 22.5 66 2 US-09-385-328-10 Sequence 10, Appli
37 161 18.3 37 1 US-08-313-681A-6 Sequence 6, Appli
38 161 18.3 37 2 US-09-322-911-6 Sequence 6, Appli
39 154 17.5 36 2 US-09-385-328-11 Sequence 11, Appli
40 133 15.1 27 2 US-09-276-202-8 Sequence 8, Appli
41 125 14.2 27 2 US-09-276-202-2 Sequence 2, Appli
42 118 13.4 27 2 US-09-276-202-3 Sequence 3, Appli
43 117 13.3 24 2 US-09-276-202-10 Sequence 10, Appli
44 117 13.3 27 2 US-09-276-202-4 Sequence 4, Appli
45 113 12.9 23 2 US-09-276-202-11 Sequence 11, Appli

ALIGNMENTS

RESULT 1

US-08-313-681A-2

; Sequence 2, Application US/08313681A

; Patent No. 5618675

; GENERAL INFORMATION:

; APPLICANT: Larrick, James W.

; APPLICANT: Wright, Susan C.

; APPLICANT: Hirata, Michimasa

; TITLE OF INVENTION: Human Cationic Proteins Having

; TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Kourie and Crew

; STREET: One Market Plaza, Steuart Tower, Suite 2000

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94105

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/313,681A

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Heslin, James M.

; REGISTRATION NUMBER: 29,541

; REFERENCE/DOCKET NUMBER: 15325-9-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-326-2400

; TELEFAX: 415-326-2422

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 170 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-313-681A-2

Query Match 100.0%; Score 879; DB 1; Length 170;

Best Local Similarity 100.0%; Pred. No. 1.1e-95;

Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTQDGHSLGRWSLVLLLLGLVMP L A I A QVLSYKEAVLR A I D G I N Q R S S D A N I Y R L L D 60

DB 1 MKTQDGHSLGRWSLVLLLLGLVMP L A I A QVLSYKEAVLR A I D G I N Q R S S D A N I Y R L L D 60

Qy 61 LDRPTMDGDDPTPKPVSFTVKETVCPRTTQOSPEDCDFKKDGLVKRCMGTTVLNQARGS 120
Db 61 LDRPTMDGDDPTPKPVSFTVKETVCPRTTQOSPEDCDFKKDGLVKRCMGTTVLNQARGS 120
Qy 121 FDISCDKDKRKFALLGDFFRKSKKIGKFKRIVQRIKDFLNLVPRTES 170
Db 121 FDISCDKDKRKFALLGDFFRKSKKIGKFKRIVQRIKDFLNLVPRTES 170

RESULT 2
US-09-322-911-2
; Sequence 2, Application US/09322911
; Patent No. 6103888
; GENERAL INFORMATION:
; APPLICANT: Larrick, James W.
; APPLICANT: Wright, Susan C.
; APPLICANT: Hirata, Mishimasa
; APPLICANT: Balint, Robert F.
; TITLE OF INVENTION: Human Cationic Proteins Having
; TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/322,911
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/691,280
; FILING DATE: August 1, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/916,761
; FILING DATE: July 17, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/916,765
; FILING DATE: July 17, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06731
; FILING DATE: July 15, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/313,681
; FILING DATE: September 27, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fittle, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 15325-000920
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-322-911-2

Query Match 100.0%; Score 879; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.1e-95;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKTORDGHSIGRWSLVLLLLGLVNPPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
Db 1 MKTORDGHSIGRWSLVLLLLGLVNPPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
Qy 61 LDRPTMDGDDPTPKPVSFTVKETVCPRTTQOSPEDCDFKKDGLVKRCMGTTVLNQARGS 120
Db 61 LDRPTMDGDDPTPKPVSFTVKETVCPRTTQOSPEDCDFKKDGLVKRCMGTTVLNQARGS 120
Qy 121 FDISCDKDKRKFALLGDFFRKSKKIGKFKRIVQRIKDFLNLVPRTES 170
Db 121 FDISCDKDKRKFALLGDFFRKSKKIGKFKRIVQRIKDFLNLVPRTES 170

RESULT 3
US-09-917-340-32
; Sequence 32, Application US/09917340
; Patent No. 6696238
; GENERAL INFORMATION:
; APPLICANT: Murphy, Christopher J.
; APPLICANT: McAnulty, Jonathan F.
; APPLICANT: Reid, Ted W.
; TITLE OF INVENTION: Transplant Media
; FILE REFERENCE: TELANT-06468
; CURRENT APPLICATION NUMBER: US/09/917,340
; CURRENT FILING DATE: 2001-07-29
; PRIOR APPLICATION NUMBER: 60/221,632
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/290,932
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-917-340-32

Query Match 99.4%; Score 874; DB 2; Length 170;
Best Local Similarity 99.4%; Pred. No. 4.3e-95;
Matches 169; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKTORDGHSIGRWSLVLLLLGLVNPPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
Db 1 MKTORDGHSIGRWSLVLLLLGLVNPPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
Qy 61 LDRPTMDGDDPTPKPVSFTVKETVCPRTTQOSPEDCDFKKDGLVKRCMGTTVLNQARGS 120
Db 61 LDRPTMDGDDPTPKPVSFTVKETVCPRTTQOSPEDCDFKKDGLVKRCMGTTVLNQARGS 120
Qy 121 FDISCDKDKRKFALLGDFFRKSKKIGKFKRIVQRIKDFLNLVPRTES 170
Db 121 FDISCDKDKRKFALLGDFFRKSKKIGKFKRIVQRIKDFLNLVPRTES 170

RESULT 4
US-09-513-999C-7862
; Sequence 7862, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm

; SEQ ID NO 7862
; LENGTH: 152

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SIGNAL

; LOCATION: -33...-1

; OTHER INFORMATION: score 9.5

; OTHER INFORMATION: seq LLLGLVPLAIIA/QV

US-09-513-999C-7862

Query Match 86.6%; Score 761; DB 2; Length 152;

Best Local Similarity 98.6%; Pred. No. 8.2e-82;

Matches 146; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKTORDGHSGLRWSLVLLLLGLVPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60

DB 4 MKTORDGHSGLRWSLVLLLLGLVPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 63

QY 61 LDPRTMDGDDPTPKVSVTVKTCVPRTTQOSPEDCDPKDGLVKRCMGTVTLNQARGS 120

DB 64 LDPRTMDGDDPTPKVSVTVKTCVPRTTQOSPEDCDPKDGLVKRCMGTVTLNQARGS 123

QY 121 FDISCDKDKRFFALLGDFPRKSKKIGK 148

DB 124 FDISCDKDKRFFALLGDFPRKSKKMAK 151

RESULT 5

US-08-313-681A-4

; Sequence 4, Application US/08313681A

; Patent No. 5618675

; GENERAL INFORMATION:

; APPLICANT: Larrick, James W.

; APPLICANT: Wright, Susan C.

; APPLICANT: Hirata, Mishimasa

; TITLE OF INVENTION: Human Cationic Proteins Having

; TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESS: Townsend and Townsend Kourie and Crew

; STREET: One Market Plaza, Steuart Tower, Suite 2000

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94105

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/313,681A

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Heslin, James M.

; REGISTRATION NUMBER: 29,541

; REFERENCE/DOCKET NUMBER: 15325-9-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-326-2400

; TELEFAX: 415-326-2422

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 171 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-313-681A-4

Query Match

Best Local Similarity 53.0%; Score 465.5; DB 1; Length 171;

Matches 146; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Matches 98; Conservative 26; Mismatches 44; Indels 3; Gaps 2;

QY 1 MKTORDGHSGLRWSLVLLLLGLVPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60

DB 1 METHKHGPSLAWWSLLLLGLLMLPPA-IAQDLTYREAVLRAVDAPNQSSSEANLYRLLS 59

QY 61 LDPRTMDGDDPTPKVSVTVKTCVPRTTQOSPEDCDPKDGLVKRCMGTVTLNQARGS 120

DB 60 MDPOQLEDAKPYTPQVSVTVKTCVPRTTQOSPEDCDPKDGLVKRCMGTVTRYQAWDS 119

QY 121 FDISCDK--DNKRFFALLGDFPRKSKKIGKSKRIVQRIKDFLRNLVPRTE 169

DB 120 FDIRCNRAQESPEPTGLRKRLKRPKNKEKLLKXKIQGLLPKLAPRTD 170

RESULT 6

US-09-322-911-4

; Sequence 4, Application US/09322911

; Patent No. 6103888

; GENERAL INFORMATION:

; APPLICANT: Larrick, James W.

; APPLICANT: Wright, Susan C.

; APPLICANT: Hirata, Mishimasa

; APPLICANT: Balint, Robert F.

; TITLE OF INVENTION: Human Cationic Proteins Having

; TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESS: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, 8th Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/322,911

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/691,280

; FILING DATE: August 1, 1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/916,761

; FILING DATE: July 17, 1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/916,765

; FILING DATE: July 17, 1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US93/06731

; FILING DATE: July 15, 1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/313,681

; FILING DATE: September 27, 1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Fitts, Renee A.

; REGISTRATION NUMBER: 35,136

; REFERENCE/DOCKET NUMBER: 15325-000920

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-326-2400

; TELEFAX: 415-326-2422

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 171 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-322-911-4

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; PRIOR APPLICATION NUMBER: 60/221,632
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/290,932
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Equus asinus
US-09-917-340-35

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| Qy | | | | |
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| 1 | METQRTNRCIGRWSPGLLLGLVTPPA | TTQALS YKEAVLR | ADGINORSSDENLYRLLE | 59 |
| Db | | | | |
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| 61 | LDRPRTWMDGPDPTPKPVSVFTVKETV | CBRTQQSPEDCDFKDG | LWKRCMGVTTLNQARGS | 120 |
| Qy | | | | |
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| 60 | LDLPLPKGDKSDPTPKPVSVFVKETVC | PRIMKQTEPCQCD | FKENGVLKQCVGTILGFVKDH | 119 |
| Db | | | | |
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| 121 | FDLSCDKDN--KRFALLGDFFRKSKEKIG | KEFKRIVORIKDFLRNLVPR | 167 | |
| Qy | | | | |
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| 120 | FDVSCGSPORVKRFG----- | RLAKSFLE----- | MRILLPR | 149 |
| Db | | | | |
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; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/290,932
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-917-340-34

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| Qy | 1 | MTKORDGHSIGRWSLVLLLLGLVMPPLAI | IAQVLSYKEAVLRRAIDGINORSSDANLYRLLD | 60 |
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| Db | 1 | METQRASLSIGRWSLWLLLLGLALPSA | SAQALSRYREAVLRVAVDLQNEKSSSEANLYRLLE | 59 |
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| Qy | 61 | LDPRPTWDGD | PDTFKVSVSTVKEITCPRITQOSPEDCDFKKGDLVKECMGTVTLLNQAAG | 119 |
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| Db | 60 | LDPPPKEDDENPFIKVPSPRVKRTVCPTSSQQSP | QEQCDFKENGLLKKECVGTIVLDQVGS | 119 |
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| Qy | 120 | SFDISC | 125 | |
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| Db | 120 | NFDITC | 125 | |
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RESULT 10
 US-09-917-340-29
 ; Sequence 29, Application US/09917340
 ; Patent No. 6696238
 ; GENERAL INFORMATION:
 ; APPLICANT: Murphy, Christopher J.
 ; APPLICANT: McAuley, Jonathan P.
 ; APPLICANT: Reid, Ted W.
 ; TITLE OF INVENTION: Transplant Media
 ; FILE REFERENCE: TPLANT-06468
 ; CURRENT APPLICATION NUMBER: US/09/917,340
 ; CURRENT FILING DATE: 2001-07-29
 ; PRIOR APPLICATION NUMBER: 60/221,632
 ; PRIOR FILING DATE: 2000-07-28
 ; PRIOR APPLICATION NUMBER: 60/249,602
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/290,932
 ; PRIOR FILING DATE: 2001-05-15
 ; NUMBER OF SEQ ID NOS: 96
 ; SOFTWARE: Patent in Ver. 2.0
 ; SEQ ID NO 29
 ; LENGTH: 155
 ; TYPE: PRT
 ; ORGANISM: Bos taurus
 ; US-09-917-340-29

Query Match 48.6%; Score 427.5; DB 2; Length 155;
 Best Local Similarity 66.7%; Pred. No. 2.1e-42;
 Matches 84; Conservative 18; Mismatches 23; Indels 1; Gaps 1;
 QY 1 MKTQRDGHSLGRWSLVLLLLGLVMPLEIAIQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
 DB 1 METPRASLGLRWSLVLLLLGLALPSA-SQAQLSYREAVLRAVDQNLQSESPNIYRLLE 59
 QY 61 LDPRPTMDGDDPTPKPVSFTVKETVCPRTTQOSPEDCFKDDGLVKRCMGTTVLNQARGS 120
 DB 60 LDQPPQDDEDDPSKRVSRVKTVCSTTQPPPEQCFKNGLLKRCGEGTTLQDVRGN 119
 QY 121 FDISCDK 126
 DB 120 FDIICN 125

RESULT 11
 US-08-243-879A-38
 ; Sequence 38, Application US/08243879A
 ; Patent No. 5708145
 ; GENERAL INFORMATION:
 ; APPLICANT: LEHRER, ROBERT I.
 ; APPLICANT: HARWIG, SYLVIA S.L.
 ; TITLE OF INVENTION: A NEW PROTEGRIN
 ; NUMBER OF SEQUENCES: 42
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
 ; CITY: Washington, DC
 ; COUNTRY: USA
 ; ZIP: 20006-1812
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/243,879A
 ; FILING DATE: 17-MAY-1994
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MURASHIGE, KATE H.
 ; REGISTRATION NUMBER: 29,959
 ; REFERENCE/DOCKET NUMBER: 2000-0540.22
 ; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 887-1500
 ; TELEFAX: (202) 887-0763
 ; TELEX: 90-4030
 ; INFORMATION FOR SEQ ID NO: 38:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 147 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-243-879A-38

Query Match 47.6%; Score 418.5; DB 1; Length 147;
 Best Local Similarity 65.4%; Pred. No. 2.3e-41;
 Matches 83; Conservative 19; Mismatches 24; Indels 1; Gaps 1;
 QY 1 MKTQRDGHSLGRWSLVLLLLGLVMPLEIAIQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
 DB 1 METQRASLCLGRWSLVLLLLGLALVPSA-SQAQLSYREAVLRAVDRLNEQSEANLYRLLE 59
 QY 61 LDPRPTMDGDDPTPKPVSFTVKETVCPRTTQOSPEDCFKDDGLVKRCMGTTVLNQARGS 120
 DB 60 LDQPPKADEDFETPKPVSFTVKETVCPRTTRQPPPELCDFKENGVRKQCVGTTLQDKDP 119
 QY 121 FDISCDK 127
 DB 120 LDITCNE 126

RESULT 12
 US-08-499-523-4
 ; Sequence 4, Application US/08499523
 ; Patent No. 5804558
 ; GENERAL INFORMATION:
 ; APPLICANT: LEHRER, ROBERT I.
 ; APPLICANT: HARWIG, SYLVIA S.L.
 ; APPLICANT: KOKRYAKOV, VLADIMIR N.
 ; TITLE OF INVENTION: PROTEGRINS
 ; NUMBER OF SEQUENCES: 76
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20006-1812
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/499,523
 ; FILING DATE: 07-JUL-1995
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MURASHIGE, KATE H.
 ; REGISTRATION NUMBER: 29,959
 ; REFERENCE/DOCKET NUMBER: 2000-0540.24
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 887-1500
 ; TELEFAX: (202) 887-0763
 ; TELEX: 90-4030
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 147 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-499-523-4

Query Match 47.6%; Score 418.5; DB 1; Length 147;
 Best Local Similarity 65.4%; Pred. No. 2.3e-41;
 Matches 83; Conservative 19; Mismatches 24; Indels 1; Gaps 1;

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Qy 1 MTKTQDGHSLGRWSLVLLLLGLVMPALIAIQVLSYKEAVLRDAIDGINQRSDANLVRLLD 60
Db 1 METQRASLCLGRWSLWLLLLALVWPSA-SQAQLSYREAVLRADVRLNEQSSEANLYRLLE 59

Qy 61 LDRPTMDGDDPTPKVPSFTVKTCTTQGSPEDCDFKQGLGLVKRCMGTVTLNQARGS 120
Db 60 LDQPPKADPDGPTPKVPSFTVKTCTTQGSPEDCDFKQGLGLVKRCMGTVTLNQARGS 119

Qy 121 FDISCDK 127
Db 120 LDITCNE 126

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RESULT 13
US-09-128-345-4
Sequence 4, Application US/09128345
Patent No. 6159936
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: KARWIG, SYLVIA S.L.
APPLICANT: KORZYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128/345

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|-----------------------|--------|---|----------------|-------------------|
| Query Match | 47.6%; | Score 418.5; | DB 2; | Length 147; |
| Best Local Similarity | 65.4%; | Pred. No. 2.3e-41; | | |
| Matches | 83; | Conservative 19; | Mismatches 24; | Indels 1; Gaps 1; |
| Qy | 1 | MKTORDGHSIGRWSLVLLGLGLVMPALIIAQVLVSKEAVLRAIDGINQRSSDANLYRLLD | 60 | |
| Db | 1 | METORASLCIGRWSLWLLLLALVVPSPA-SQAQLSYRAVLRAVDRLNEQSEANLYRLE | 59 | |
| Qy | 61 | LDPRPTWGDGPPDTPKPSVFTVKETVCPRPTQOSPEDCDFKXDGVLVXGCMGVTVTLLNQARS | 120 | |
| Db | 60 | LDQPPKADEPGTTPKPSVFTVKETVCPRPTQPELCDFKENGGRVKQCVGVTLLDQIKDP | 119 | |
| Qy | 121 | FDISCDK | 127 | |
| Db | 120 | LDITCNE | 126 | |

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|-----------------------|------------------|--|-----------|-------------|
| Query Match | 47.6% | Score 418.5; | DB 1; | Length 149; |
| Best Local Similarity | 65.4%; | Pred. No. 2.3e-41; | | |
| Matches 83; | Conservative 19; | Mismatches 24; | Indels 1; | Gaps 1; |
| Qy | 1 | MKTORDGHSIGRWSLVLLILGLVMPYLAIIQAQVLSYKEAVLRAIDGINORSSDANLYRLLD | 60 | |
| Db | 1 | METQRASLCIGRWSLWLLLLALVPPSA-SAAQUSYREAVLRVDRLNEQSSEANLYRLE | 59 | |
| Qy | 61 | LDERPTMDGDPDTPKPVSVFTKVTCTPRTTQQSPEDCDFFKQGLVKRCMGTVTLNQARGS | 120 | |
| Db | 60 | LDQPPKADEDPGTGFKPVSVFTKVTCTPRTQPELCDPFGKNGRVKQCVGTVTLLDQIKDP | 119 | |
| Qy | 121 | FDISCDK | 127 | |
| Db | 120 | LDITCNE | 126 | |

RESULT 15
US-08-243-879A-40
; Sequence 40, Application US/08243879A
; Patent No. 5708145
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S.L.
; TITLE OF INVENTION: A NEW PROTEGRIN
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FORSTER
; STREET: 2000 Pennsylvania Ave. N.
; CITY: Washington, DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,879A
FILING DATE: 17-MAY-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0540.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030

INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 149 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-243-879A-40

Query Match 47.6%; Score 418.5; DB 1; Length 149;
Best Local Similarity 65.4%; Pred. No. 2.3e-41;
Matches 83; Conservative 19; Mismatches 24; Indels 1; Gaps 1;

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| Qy | 1 | MKTORDGHSGLGRWSLVLALLGLVMPLEIIAQVLSYKEAVLRALDGINORSSDANLYRLLD | 60 |
| Db | 1 | METQASLCGLGRWSLWLLLLLVVPSA-SAQALSYREAVLRADRLNEQSSSEANLYRLLE | 59 |
| Qy | 61 | LDPRPTMDGDPDTPKPVSVFTVKETVCPRTTQSPEDCDPKDGLVKRCMGTVTLNQARGS | 120 |
| Db | 60 | LDQPPKADEDPGTPKPVSVFTVKETVCPRTTRQPPPELCPDKENGVRKQCVGTTLQIKDP | 119 |
| Qy | 121 | FDISCDK | 127 |
| Db | 120 | LDITCNE | 126 |

Search completed: January 12, 2006, 21:51:59
Job time : 26.3469 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 12, 2006, 21:45:40 ; Search time 70.2583 Seconds
(without alignments)
1010.998 Million cell updates/sec

Title: US-10-815-562-2
Perfect score: 879
Sequence: 1 MKTQDGHSLGRWSLVLLLL.....KRIYQIKDFLNLVPRTES 170

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA_Main:
1: /cgm2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgm2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgm2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgm2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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6: /cgm2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|---------------------|
| 1 | 879 | 100.0 | 170 | 4 | US-10-603-566-51 |
| 2 | 879 | 100.0 | 170 | 5 | US-10-893-485-51 |
| 3 | 874 | 99.4 | 170 | 3 | US-09-917-340-32 |
| 4 | 874 | 99.4 | 170 | 5 | US-10-844-837-32 |
| 5 | 874 | 99.4 | 170 | 5 | US-10-777-683-4 |
| 6 | 874 | 99.4 | 170 | 5 | US-10-909-119-47 |
| 7 | 874 | 99.4 | 170 | 5 | US-10-657-851-32 |
| 8 | 874 | 99.4 | 170 | 5 | US-10-287-436A-513 |
| 9 | 874 | 99.4 | 170 | 5 | US-10-287-436A-1204 |
| 10 | 865 | 98.4 | 170 | 4 | US-10-344-709C-11 |
| 11 | 468.5 | 53.3 | 171 | 4 | US-10-344-709C-7 |
| 12 | 457.5 | 52.0 | 170 | 3 | US-09-917-340-33 |
| 13 | 457.5 | 52.0 | 170 | 5 | US-10-844-837-33 |
| 14 | 457.5 | 52.0 | 170 | 5 | US-10-909-119-48 |
| 15 | 457.5 | 52.0 | 170 | 5 | US-10-657-851-33 |
| 16 | 451 | 51.3 | 156 | 3 | US-09-917-340-35 |
| 17 | 451 | 51.3 | 156 | 5 | US-10-844-837-35 |
| 18 | 451 | 51.3 | 156 | 5 | US-10-909-119-50 |
| 19 | 451 | 51.3 | 156 | 5 | US-10-657-851-35 |
| 20 | 432 | 49.1 | 159 | 3 | US-09-917-340-34 |
| 21 | 432 | 49.1 | 159 | 5 | US-10-844-837-34 |
| 22 | 432 | 49.1 | 159 | 5 | US-10-909-119-49 |
| 23 | 432 | 49.1 | 159 | 5 | US-10-657-851-34 |
| 24 | 431.5 | 49.1 | 173 | 4 | US-10-344-709C-5 |
| 25 | 427.5 | 48.6 | 155 | 3 | US-09-917-340-29 |
| 26 | 427.5 | 48.6 | 155 | 4 | US-10-344-709C-8 |
| 27 | 427.5 | 48.6 | 155 | 5 | US-10-844-837-29 |

| | | | | | | |
|----|-------|------|-----|---|------------------|-------------------|
| 28 | 427.5 | 48.6 | 155 | 5 | US-10-909-119-44 | Sequence 44, Appl |
| 29 | 427.5 | 48.6 | 155 | 5 | US-10-657-851-29 | Sequence 29, Appl |
| 30 | 418.5 | 47.6 | 147 | 3 | US-09-539-443-4 | Sequence 4, Appl |
| 31 | 418.5 | 47.6 | 147 | 4 | US-10-627-829-4 | Sequence 4, Appl |
| 32 | 418.5 | 47.6 | 149 | 3 | US-09-539-443-2 | Sequence 2, Appl |
| 33 | 418.5 | 47.6 | 149 | 3 | US-09-539-443-6 | Sequence 6, Appl |
| 34 | 418.5 | 47.6 | 149 | 3 | US-09-539-443-8 | Sequence 8, Appl |
| 35 | 418.5 | 47.6 | 149 | 3 | US-09-539-443-10 | Sequence 10, Appl |
| 36 | 418.5 | 47.6 | 149 | 4 | US-10-627-829-2 | Sequence 2, Appl |
| 37 | 418.5 | 47.6 | 149 | 4 | US-10-627-829-6 | Sequence 6, Appl |
| 38 | 418.5 | 47.6 | 149 | 4 | US-10-627-829-8 | Sequence 8, Appl |
| 39 | 418.5 | 47.6 | 149 | 4 | US-10-627-829-10 | Sequence 10, Appl |
| 40 | 413 | 47.0 | 158 | 5 | US-10-485-278-8 | Sequence 8, Appl |
| 41 | 412 | 46.9 | 160 | 3 | US-09-917-340-36 | Sequence 36, Appl |
| 42 | 412 | 46.9 | 160 | 5 | US-10-844-837-36 | Sequence 36, Appl |
| 43 | 412 | 46.9 | 160 | 5 | US-10-909-119-51 | Sequence 51, Appl |
| 44 | 412 | 46.9 | 160 | 5 | US-10-657-851-36 | Sequence 36, Appl |
| 45 | 410.5 | 46.7 | 176 | 3 | US-09-917-340-28 | Sequence 28, Appl |

ALIGNMENTS

RESULT 1
US-10-603-566-51
; Sequence 51, Application US/10603566
; Publication No. US20040086966A1
; GENERAL INFORMATION:
; APPLICANT: Wittamer, Valerie
; APPLICANT: Communi, David
; APPLICANT: Vandenberghe, Ann
; APPLICANT: Dethoux, Michel
; APPLICANT: Parmentier, Marc
; TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of ChemerinR
; FILE REFERENCE: 9409/2212
; CURRENT APPLICATION NUMBER: US/10/603,566
; CURRENT FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US 60/303,858
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 09/905,253
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 10/201,187
; PRIOR FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-603-566-51
Query Match 100.0%; Score 879; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.7e-87;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKTQDGHSLGRWSLVLLLLGLVMP LAIIAQVLSYKEAVLRAIDGINS DANLYRLLD 60
Db 1 MKTQDGHSLGRWSLVLLLLGLVMP LAIIAQVLSYKEAVLRAIDGINS DANLYRLLD 60
QY 61 LDPRTMGDDPTPKPVSTFKETVCPRTTQSPEDCDPKDGLVKRCMGTVTLLNQARGS 120
Db 61 LDPRTMGDDPTPKPVSTFKETVCPRTTQSPEDCDPKDGLVKRCMGTVTLLNQARGS 120
QY 121 FDISCDKNKRFALLGDPFRKSKKEKIGFKRIQRIKDFLNLVPRTES 170
Db 121 FDISCDKNKRFALLGDPFRKSKKEKIGFKRIQRIKDFLNLVPRTES 170
RESULT 2
US-10-893-485-51
; Sequence 51, Application US/10893485
; Publication No. US20050155090A1
; GENERAL INFORMATION:

```

; APPLICANT: Wittamer, Valerie
; APPLICANT: Communi, David
; APPLICANT: Vandenbogaerde, Ann
; APPLICANT: Dethieux, Michel
; APPLICANT: Parmentier, Marc
; TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of Chemerin
; FILE REFERENCE: 9409/2045C
; CURRENT APPLICATION NUMBER: US/10/893,485
; CURRENT FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: US 60/303,858
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US10/603,566
; PRIOR FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US 09/905,253
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 10/201,187
; PRIOR FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-893-485-51

Query Match          100.0%; Score 879; DB 5; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.7e-87;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MKTQRDGHSLGRWSLVLLLLGLVPLAIIAQVLSYKEAVLRAIDGINORSSDANLYRLLD 60
Db      1  MKTQRDGHSLGRWSLVLLLLGLVPLAIIAQVLSYKEAVLRAIDGINORSSDANLYRLLD 60

Qy      61  LDRPRTMGDGDPDPKPVSVTVKTEVCPRTTQOSPEDCPKDGKGLVKRCMGTVTLNQARGS 120
Db      61  LDRPRTMGDGDPDPKPVSVTVKTEVCPRTTQOSPEDCPKDGKGLVKRCMGTVTLNQARGS 120

Qy      121  FDISCDKNKRFALLGDFPRKSKKEIKGFKRIVORIKDFLRNLVPTRES 170
Db      121  FDISCDKNKRFALLGDFPRKSKKEIKGFKRIVORIKDFLRNLVPTRES 170

RESULT 3
US-09-917-340-32
; Sequence 32, Application US/09917340
; Patent No. US20020090369A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Christopher J.
; APPLICANT: McAnulty, Jonathan F.
; APPLICANT: Reid, Ted W.
; TITLE OF INVENTION: Transplant Media
; FILE REFERENCE: TPLANT-06468
; CURRENT APPLICATION NUMBER: US/09/917,340
; CURRENT FILING DATE: 2001-07-29
; PRIOR APPLICATION NUMBER: 60/221,632
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/290,932
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-917-340-32

Query Match          99.4%; Score 874; DB 3; Length 170;
Best Local Similarity 99.4%; Pred. No. 5.9e-87;
Matches 169; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MKTQRDGHSLGRWSLVLLLLGLVPLAIIAQVLSYKEAVLRAIDGINORSSDANLYRLLD 60

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Matches 169; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKTQDGHSLGRWSLVLLGLVMPPLAIIAQLVSYKEAVLRAIDGINQRSSDANLYRLLD 60
DB 1 MKTQNGHSLGRWSLVLLGLVMPPLAIIAQLVSYKEAVLRAIDGINQRSSDANLYRLLD 60
QY 61 LDPRTMDGDDPTPKVSVFTVKETVCPRTTQSPEDCDPKDGLVKRCMGTVTLLNQARGS 120
DB 61 LDPRTMDGDDPTPKVSVFTVKETVCPRTTQSPEDCDPKDGLVKRCMGTVTLLNQARGS 120
QY 121 FDISCDKDKRFPALLGDFPRKSKKIGKEFKRIVQRIKDFLRNLVPRTES 170
DB 121 FDISCDKDKRFPALLGDFPRKSKKIGKEFKRIVQRIKDFLRNLVPRTES 170

RESULT 6
US-10-909-119-47
; Sequence 47, Application US/10909119
; Publication No. US20050079578A1
; GENERAL INFORMATION:
; APPLICANT: Centanni, John M.
; TITLE OF INVENTION: Human Skin Equivalents Expressing Exogenous Polypeptides
; FILE REFERENCE: STRATA-09123
; CURRENT APPLICATION NUMBER: US/10/909,119
; CURRENT FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-909-119-47

Query Match 99.4%; Score 874; DB 5; Length 170;
Best Local Similarity 99.4%; Pred. No. 5.9e-87;
Matches 169; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKTQDGHSLGRWSLVLLGLVMPPLAIIAQLVSYKEAVLRAIDGINQRSSDANLYRLLD 60
DB 1 MKTQNGHSLGRWSLVLLGLVMPPLAIIAQLVSYKEAVLRAIDGINQRSSDANLYRLLD 60
QY 61 LDPRTMDGDDPTPKVSVFTVKETVCPRTTQSPEDCDPKDGLVKRCMGTVTLLNQARGS 120
DB 61 LDPRTMDGDDPTPKVSVFTVKETVCPRTTQSPEDCDPKDGLVKRCMGTVTLLNQARGS 120
QY 121 FDISCDKDKRFPALLGDFPRKSKKIGKEFKRIVQRIKDFLRNLVPRTES 170
DB 121 FDISCDKDKRFPALLGDFPRKSKKIGKEFKRIVQRIKDFLRNLVPRTES 170

RESULT 7
US-10-657-851-32
; Sequence 32, Application US/10657851
; Publication No. US20050089836A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Christopher J.
; APPLICANT: McAulity, Jonathan P.
; APPLICANT: Reid, Ted W.
; TITLE OF INVENTION: Transplant Media
; FILE REFERENCE: TPLANT-06468
; CURRENT APPLICATION NUMBER: US/10/657,851
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: US/09/917,340
; PRIOR FILING DATE: 2001-07-29
; PRIOR APPLICATION NUMBER: 60/221,632
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/290,932
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 32
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-657-851-32

Query Match 99.4%; Score 874; DB 5; Length 170;
Best Local Similarity 99.4%; Pred. No. 5.9e-87;
Matches 169; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKTQDGHSLGRWSLVLLGLVMPPLAIIAQLVSYKEAVLRAIDGINQRSSDANLYRLLD 60
DB 1 MKTQNGHSLGRWSLVLLGLVMPPLAIIAQLVSYKEAVLRAIDGINQRSSDANLYRLLD 60
QY 61 LDPRTMDGDDPTPKVSVFTVKETVCPRTTQSPEDCDPKDGLVKRCMGTVTLLNQARGS 120
DB 61 LDPRTMDGDDPTPKVSVFTVKETVCPRTTQSPEDCDPKDGLVKRCMGTVTLLNQARGS 120
QY 121 FDISCDKDKRFPALLGDFPRKSKKIGKEFKRIVQRIKDFLRNLVPRTES 170
DB 121 FDISCDKDKRFPALLGDFPRKSKKIGKEFKRIVQRIKDFLRNLVPRTES 170

RESULT 8
US-10-287-436A-513
; Sequence 513, Application US/10287436A
; Publication No. US20050202421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 513
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-436A-513

Query Match 99.4%; Score 874; DB 5; Length 170;
Best Local Similarity 99.4%; Pred. No. 5.9e-87;
Matches 169; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKTQDGHSLGRWSLVLLGLVMPPLAIIAQLVSYKEAVLRAIDGINQRSSDANLYRLLD 60
DB 1 MKTQNGHSLGRWSLVLLGLVMPPLAIIAQLVSYKEAVLRAIDGINQRSSDANLYRLLD 60
QY 61 LDPRTMDGDDPTPKVSVFTVKETVCPRTTQSPEDCDPKDGLVKRCMGTVTLLNQARGS 120
DB 61 LDPRTMDGDDPTPKVSVFTVKETVCPRTTQSPEDCDPKDGLVKRCMGTVTLLNQARGS 120
QY 121 FDISCDKDKRFPALLGDFPRKSKKIGKEFKRIVQRIKDFLRNLVPRTES 170
DB 121 FDISCDKDKRFPALLGDFPRKSKKIGKEFKRIVQRIKDFLRNLVPRTES 170

RESULT 9
US-10-287-436A-1204
; Sequence 1204, Application US/10287436A
; Publication No. US20050202421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
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; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1204
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-436A-1204

Query Match          99.4%; Score 874; DB 5; Length 170;
Best Local Similarity 99.4%; Pred. No. 5.9e-87;
Matches 169; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTQDGHSLGRWSLVLLLLGLVMPALIAIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MKTQDGHSLGRWSLVLLLLGLVMPALIAIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60

QY 61 LDPRTMDGDDPTPKPVSVTKVETVCPRTTQOSPEDCDPKDGLVKRCMGTVTLNQARGS 120
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Db 61 LDPRTMDGDDPTPKPVSVTKVETVCPRTTQOSPEDCDPKDGLVKRCMGTVTLNQARGS 120

QY 121 FDISCDKDKRFPALLGDFPRKSKKIGKEFKRIVQRIKDFLRNLVPRTES 170
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 FDISCDKDKRFPALLGDFPRKSKKIGKEFKRIVQRIKDFLRNLVPRTES 170

RESULT 10
US-10-344-709C-11
; Sequence 11, Application US/10344709C
; Publication No. US20040170642A1
; GENERAL INFORMATION:
; APPLICANT: JORG FRITZ ET AL.
; TITLE OF INVENTION: Vaccine which comprises at least one antigen and a cathelicidin
; FILE REFERENCE: SONN:030US
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: PCT/EP01/09529
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: A 1416/2000
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
US-10-344-709C-11

Query Match          98.4%; Score 865; DB 4; Length 170;
Best Local Similarity 98.8%; Pred. No. 5.7e-86;
Matches 168; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKTQDGHSLGRWSLVLLLLGLVMPALIAIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MKTQDGHSLGRWSLVLLLLGLVMPALIAIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60

QY 61 LDPRTMDGDDPTPKPVSVTKVETVCPRTTQOSPEDCDPKDGLVKRCMGTVTLNQARGS 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 LDPRTMDGDDPTPKPVSVTKVETVCPRTTQOSPEDCDPKDGLVKRCMGTVTLNQARGS 120

QY 121 FDISCDKDKRFPALLGDFPRKSKKIGKEFKRIVQRIKDFLRNLVPRTES 170
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 FDISCDKDKRFPALLGDFPRKSKKIGKEFKRIVQRIKDFLRNLVPRTES 170

RESULT 11
US-10-344-709C-7
; Sequence 7, Application US/10344709C
; Publication No. US20040170642A1
; GENERAL INFORMATION:
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; APPLICANT: JORG FRITZ ET AL.
; TITLE OF INVENTION: Vaccine which comprises at least one antigen and a cathelicidin
; FILE REFERENCE: SONN:030US
; CURRENT APPLICATION NUMBER: US/10/344,709C
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: PCT/EP01/09529
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: A 1416/2000
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
US-10-344-709C-7

Query Match          53.3%; Score 468.5; DB 4; Length 171;
Best Local Similarity 57.3%; Pred. No. 1.2e-42;
Matches 98; Conservative 27; Mismatches 43; Indels 3; Gaps 2;

QY 1 MKTQDGHSLGRWSLVLLLLGLVMPALIAIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 METHKHGPSLAWWSLILLLLGLLMPPA-IAQDLTYREAVLRAVDADFNAFQQSSEANLYRLLS 59

QY 61 LDPRTMDGDDPTPKPVSVTKVETVCPRTTQOSPEDCDPKDGLVKRCMGTVTLNQARGS 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 MDPQOLEDAPYTFQPVSVTKVETVCPRTTQOSPEDCDPKDGLVKRCMGTVTLNQARGS 119

QY 121 FDISCDK--DNKRFALLGDFPRKSKKIGKEFKRIVQRIKDFLRNLVPRTE 169
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 FDIRCRAQESPEPTGLKRLKRPKNKIKEKLLKKIGKIQGFVPLAPRTD 170

RESULT 12
US-09-917-340-33
; Sequence 33, Application US/09917340
; Patent No. US20020090369A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Christopher J.
; APPLICANT: McAnulty, Jonathan F.
; APPLICANT: Reid, Ted W.
; TITLE OF INVENTION: Transplant Media
; FILE REFERENCE: TPLANT-08468
; CURRENT APPLICATION NUMBER: US/09/917,340
; CURRENT FILING DATE: 2001-07-29
; PRIOR APPLICATION NUMBER: 60/221,632
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/290,932
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Equus caballus
US-09-917-340-33

Query Match          52.0%; Score 457.5; DB 3; Length 170;
Best Local Similarity 57.2%; Pred. No. 1.8e-41;
Matches 95; Conservative 24; Mismatches 38; Indels 9; Gaps 3;

QY 1 MKTQDGHSLGRWSLVLLLLGLVMPALIAIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 METQRTFCLGRNSPLILLLLGLVLPFA-TTQALSYKEAVLRAVDGLNQRSSDENLYRLLE 59

QY 61 LDPRTMDGDDPTPKPVSVTKVETVCPRTTQOSPEDCDPKDGLVKRCMGTVTLNQARGS 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

| | | | |
|----|-----|--|-----|
| Db | 60 | LDLPKGDKSDTPKPVSMVKETVCPRIIMKQTPQCDPKENGLVKQCVGTVILDPMVKDY | 119 |
| QY | 121 | FDISCDKN--KRFALLGDPPFKSKBKIGKEPK-----PIVORIK | 159 |
| Db | 120 | FDASCDPEQVKRTHSVGLSGLTFORHOIMRDKSEATRHGIRIITRPK | 165 |

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RESULT 15
US-10-657-851-33
, Sequence 33, Application US/10657851
, Publication No. US2005008936A1
, GENERAL INFORMATION:
, APPLICANT: Murphy, Christopher J.
, APPLICANT: McAnulty, Jonathan F.
, APPLICANT: Reid, Ted W.
, TITLE OF INVENTION: Transplant Media
, FILE REFERENCE: TPLANT-06468
, CURRENT APPLICATION NUMBER: US/10/657,851
, CURRENT FILING DATE: 2003-09-09
, PRIOR APPLICATION NUMBER: US/09/917,340
, PRIOR FILING DATE: 2001-07-29
, PRIOR APPLICATION NUMBER: 60/221,632
, PRIOR FILING DATE: 2000-07-28
, PRIOR APPLICATION NUMBER: 60/249,602
, PRIOR FILING DATE: 2000-11-17
, PRIOR APPLICATION NUMBER: 60/290,932
, PRIOR FILING DATE: 2001-05-15
, NUMBER OF SEQ ID NOS: 96
, SOFTWARE: PatentIn Ver. 2.0
, SEQ ID NO 33
, LENGTH: 170
, TYPE: PRT
, ORGANISM: Equus caballus
US-10-657-851-33

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; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Equus caballus
;
US-10-657-851-33

Query Match          52.0%; Score 457.5; DB 5; Length 170;
Best Local Similarity 57.2%; Pred. No. 1.8e-41;
Matches 95; Conservative 24; Mismatches 38; Indels 9; Gaps 3;

QY      1  MKTQRDGHSLGRWSLVLLLLGLVPLAIAQVLVSYKEAVLRAIDGINQRSSDANLYRLLD 60
        1  METQRTNRCIGRWSPLLLLGLVTPA-TTQALSYKEAVLRAVDGLNQRSSDENLYRLLE 59
Db
QY      61  LDPRPTMDGDPTTPKPVSPFTVKTVCPTTQSQSPDCDFKQDGLVKRCMGTVTLNQARGS 120
        60  LDPLPKGDNDSTTPKPVSPFWKBTVCPRIMKQTPQCDPKENGLVKQCVGTVIDPVKDY 119
Db
QY      121  FDISCDKN--KRPALLGDFFPKSKKIKGEPK-----RIVORIK 158
        120  FPAACDPEPORVKRFHSHVSGSLIORHQIMRDKSATRHGIRIIIRPK 165
Db

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60 LDPLPKGDKSDTPKPVSEFWKVTVCPRIM
QY FDSCDKN--KRPALLGDPFKSEKIGKIGK
120 FDISCEPQVRKPSVGSLLQTHQOMLRDI

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| | | | |
|----|---|---------------------------------|----------------|
| | Query Match | 52.0%; Score 457.5; DB 5; | Length 170; |
| | Best Local Similarity | 57.2%; Pred. No. | 1.8e-41; |
| | Matches 95; | Conservative 24; | Mismatches 38; |
| | | Indels 9; | Gaps 3; |
| Qy | 1 MKTORCHSLGRWSLVLLILGLWPLAI | IAOVLSYKEAVLRADGNNORSSDANLYRLLD | 60 |
| | : : | : : | : |
| Dd | 1 METORNTRCLGRWSPLILLLGLVIPP- | -TTQAUSYKEAVLRADVGLNQRSDENLYRLE | 59 |
| Qy | 61 LDRPRTMGDGPDPFKPSFVTVKETVCPTTQQSPEDCDFFKKDLVRKCMGTVTTLNQARGS | 120 | : |

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2006, 21:48:15 ; Search time 7.52768 Seconds
(without alignments)
213.508 Million cell updates/sec

Title: US-10-815-562-2

Perfect score: 879

Sequence: 1 MKTQRDGHSLGRWSLVLLLL.....KRIVQRKDFLRNLVPTRES 170

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 67062 seqs, 9454214 residues

Total number of hits satisfying chosen parameters: 67062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /cgm2_6/ptodata/1/pubpaa/US08_NEW_PUB pep.*
- 2: /cgm2_6/ptodata/1/pubpaa/US06_NEW_PUB pep.*
- 3: /cgm2_6/ptodata/1/pubpaa/US07_NEW_PUB pep.*
- 4: /cgm2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
- 5: /cgm2_6/ptodata/1/pubpaa/US09_NEW_PUB pep.*
- 6: /cgm2_6/ptodata/1/pubpaa/US10_NEW_PUB pep.*
- 7: /cgm2_6/ptodata/1/pubpaa/US11_NEW_PUB pep.*
- 8: /cgm2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|--------------------|-------------------|
| 1 | 185 | 21.0 | 37 | US-10-985-426-9 | Sequence 9, Appli |
| 2 | 76.5 | 8.7 | 491 | US-10-793-626-406 | Sequence 406, App |
| 3 | 76.5 | 8.7 | 491 | US-10-793-626-2104 | Sequence 2104, Ap |
| 4 | 70.5 | 8.0 | 867 | US-10-131-826A-20 | Sequence 20, Appl |
| 5 | 70.5 | 8.0 | 870 | US-10-933-025-6 | Sequence 6, Appli |
| 6 | 70.5 | 8.0 | 870 | US-10-933-025-15 | Sequence 15, Appl |
| 7 | 70 | 8.0 | 645 | US-10-821-234-1409 | Sequence 1409, Ap |
| 8 | 64.5 | 7.3 | 693 | US-11-196-475-68 | Sequence 68, Appl |
| 9 | 63 | 7.2 | 325 | US-11-052-554A-356 | Sequence 356, App |
| 10 | 63 | 7.2 | 1717 | US-11-192-967-2 | Sequence 2, Appli |
| 11 | 63 | 7.2 | 1717 | US-11-193-715-2 | Sequence 8, Appli |
| 12 | 62.5 | 7.1 | 874 | US-11-012-762-8 | Sequence 198, App |
| 13 | 62 | 7.1 | 192 | US-11-033-365-198 | Sequence 200, App |
| 14 | 62 | 7.1 | 301 | US-11-033-365-200 | Sequence 362, App |
| 15 | 62 | 7.1 | 301 | US-11-074-176-362 | Sequence 254, App |
| 16 | 62 | 7.1 | 308 | US-11-074-176-254 | Sequence 20, Appl |
| 17 | 62 | 7.1 | 383 | US-10-517-939-20 | Sequence 347, App |
| 18 | 62 | 7.1 | 1061 | US-11-000-463-347 | Sequence 348, App |
| 19 | 62 | 7.1 | 1091 | US-11-000-463-348 | Sequence 15, Appl |
| 20 | 61.5 | 7.0 | 236 | US-11-100-183-15 | Sequence 17, Appl |
| 21 | 61.5 | 7.0 | 240 | US-11-100-183-17 | Sequence 1950, Ap |
| 22 | 61.5 | 7.0 | 439 | US-10-467-657-1990 | Sequence 134, App |
| 23 | 61.5 | 7.0 | 1189 | US-11-074-176-134 | Sequence 1002, Ap |
| 24 | 61.5 | 7.0 | 4495 | US-10-453-372-1002 | Sequence 42, Appl |
| 25 | 60.5 | 6.9 | 148 | US-11-174-150-42 | |

| | | | | | | |
|----|------|-----|------|---|--------------------|--------------------|
| 26 | 60.5 | 6.9 | 275 | 6 | US-10-821-234-1013 | Sequence 1013, Ap |
| 27 | 60.5 | 6.9 | 748 | 6 | US-10-467-657-8036 | Sequence 8036, Ap |
| 28 | 60.5 | 6.9 | 1166 | 6 | US-10-821-234-964 | Sequence 964, Appl |
| 29 | 60.5 | 6.9 | 1466 | 7 | US-11-186-284-33 | Sequence 33, Appl |
| 30 | 60.5 | 6.9 | 1627 | 6 | US-10-821-234-1283 | Sequence 1283, Ap |
| 31 | 60.5 | 6.9 | 3690 | 6 | US-10-995-561-1016 | Sequence 1016, Ap |
| 32 | 60.5 | 6.9 | 3714 | 6 | US-10-995-561-1015 | Sequence 1015, Ap |
| 33 | 60.5 | 6.9 | 3717 | 6 | US-10-821-234-1076 | Sequence 1076, Ap |
| 34 | 60 | 6.8 | 191 | 7 | US-11-033-365-160 | Sequence 160, App |
| 35 | 60 | 6.8 | 192 | 7 | US-11-033-365-159 | Sequence 159, App |
| 36 | 60 | 6.8 | 192 | 7 | US-11-033-365-197 | Sequence 197, App |
| 37 | 60 | 6.8 | 192 | 7 | US-11-187-522-1 | Sequence 1, Appl |
| 38 | 60 | 6.8 | 193 | 7 | US-11-033-365-196 | Sequence 196, App |
| 39 | 60 | 6.8 | 196 | 7 | US-11-033-365-199 | Sequence 199, App |
| 40 | 60 | 6.8 | 202 | 7 | US-11-144-889A-2 | Sequence 2, Appl |
| 41 | 60 | 6.8 | 241 | 7 | US-11-100-183-19 | Sequence 19, Appl |
| 42 | 60 | 6.8 | 286 | 6 | US-10-954-468-25 | Sequence 25, Appl |
| 43 | 60 | 6.8 | 287 | 6 | US-10-954-468-17 | Sequence 17, Appl |
| 44 | 60 | 6.8 | 287 | 6 | US-10-954-468-24 | Sequence 24, Appl |
| 45 | 60 | 6.8 | 288 | 6 | US-10-954-468-20 | Sequence 20, Appl |

ALIGNMENTS

RESULT 1

US-10-985-426-9
; Sequence 9, Application US/10985426
; Publication No. US20050256069A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Rajeev, Kallanthottathil G.
; TITLE OF INVENTION: IRNA AGENTS WITH BIOCLEAVABLE TETHERS
; FILE REFERENCE: 14174-099001
; CURRENT APPLICATION NUMBER: US/10/985,426
; PRIOR FILING DATE: 2004-11-09
; PRIOR APPLICATION NUMBER: US 10/916,185
; PRIOR FILING DATE: 2004-08-10
; PRIOR APPLICATION NUMBER: PCT/US2004/011829
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/465,665
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/463,772
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US 60/469,612
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/465,802
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/493,986
; PRIOR FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: US 60/494,597
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US 60/503,414
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/506,341
; PRIOR FILING DATE: 2003-09-26
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Exemplary Cell Permeation Peptides
US-10-985-426-9

Query Match 21.0%; Score 185; DB 6; Length 37;
Best Local Similarity 100.0%; Pred. No. 3.2e-14;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 LLGDFFRKSKKIKGKFKRIVQRKDFLRNLVPTRES 170

|||||

✓

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Qy 63 PRPT-----MDGDP-----DTPKPY-----SFTVK-----82
Db 365 LAPTILDIAGLDIPADMDGKSLILKLDTERPVNRFHLKKOMRWRDSDLVERGKLLHKRD 424
Qy 83 -----ETVCPRTTQ--QSPDCDFPKDGLVKRCMGTVT 113
Db 425 NDKYDAQENFLPKYQVRKVDLCQRAEYQTACEQLGQKWQCVEDATGKLK--LHKCKGPMR 482
Qy 114 LNQAR-----GSFDISCDKDKRFPALLGDFPRKSKKEKIGKEPK 151
Db 483 LGGSRALSNLVPKYYGQGSEACTCDSDGYKLSLAG----RRKKLPKKKYK 528

RESULT 5
US-10-933-025-6
; Sequence 6, Application US/10933025
; Publication No. US20050265987A1
; GENERAL INFORMATION:
; APPLICANT: ROSEN, STEFAN
; APPLICANT: HEMMERICH, STEFAN
; APPLICANT: TOMITA, MEGUMI
; TITLE OF INVENTION: Sulfotransferases and methods of use
; TITLE OF INVENTION: thereof
; FILE REFERENCE: UCAL-230CON
; CURRENT APPLICATION NUMBER: US/10/933,025
; CURRENT FILING DATE: 2004-09-01
; PRIOR APPLICATION NUMBER: 10/025,966
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/258,577
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: 60/267,831
; PRIOR FILING DATE: 2001-09-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 870
; TYPE: PRPT
; ORGANISM: Homo sapiens
US-10-933-025-6

Query March 8.0%; Score 70.5; DB 6; Length 870;
Best Local Similarity 20.4%; Pred.No. 9.1;
Matches 47; Conservative 27; Mismatches 59; Indels 97; Gaps 10

Qy 3 TORQCHSLGRWSLVLLGLVWPLAIIAQVLSYKEAVLRDAIDGINQRSSDANLYRLDLD 62
Db 315 TADGHYHIGQGLV---GKSNPYEFDIRVPPY-----VRGPNVEAGCLNPHIVLNI 364
Qy 63 PRPT-----MDGDP-----DTPKPY-----SFTVK-----82
Db 365 LAPTILDIAGLDIPADMDGKSLILKLDTERPVNRFHLKKOMRWRDSDLVERGKLLHKRD 424
Qy 83 -----ETVCPRTTQ--QSPDCDFPKDGLVKRCMGTVT 113
Db 425 NDKYDAQENFLPKYQVRKVDLCQRAEYQTACEQLGQKWQCVEDATGKLK--LHKCKGPMR 482
Qy 114 LNQAR-----GSFDISCDKDKRFPALLGDFPRKSKKEKIGKEPK 151
Db 483 LGGSRALSNLVPKYYGQGSEACTCDSDGYKLSLAG----RRKKLPKKKYK 528

RESULT 6
US-10-933-025-15
; Sequence 15, Application US/10933025
; Publication No. US20050265987A1
; GENERAL INFORMATION:
; APPLICANT: ROSEN, STEFAN
; APPLICANT: HEMMERICH, STEFAN
; APPLICANT: TOMITA, MEGUMI
; TITLE OF INVENTION: Sulfotransferases and methods of use
; TITLE OF INVENTION: thereof
; FILE REFERENCE: UCAL-230CON
; CURRENT APPLICATION NUMBER: US/10/933,025

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Db 81 TVLLEFYAPWCGCHKQFAPEYKIANILKD 110

RESULT 8

US-11-196-475-68

Sequence 68, Application US/11196475

Publication No. US20050271682A1

GENERAL INFORMATION:

APPLICANT: Dattwyler, Raymond J.

APPLICANT: Gomes Solecki, Maria J. C.

APPLICANT: Luft, Benjamin J.

APPLICANT: Dunn, John J.

TITLE OF INVENTION: Recombinant Constructs of Borrelia

TITLE OF INVENTION: Burgdorferi

FILE REFERENCE: 2631.1001-011

CURRENT APPLICATION NUMBER: US/11/196,475

PRIOR FILING DATE: 2005-08-03

PRIOR APPLICATION NUMBER: US 08/148,191

PRIOR FILING DATE: 1993-11-01

PRIOR APPLICATION NUMBER: US 08/235,836

PRIOR FILING DATE: 1994-04-29

PRIOR APPLICATION NUMBER: US 09/666,017

PRIOR FILING DATE: 2000-09-19

PRIOR APPLICATION NUMBER: US 60/226,484

PRIOR FILING DATE: 2000-08-18

PRIOR APPLICATION NUMBER: PCT/US01/24736

PRIOR FILING DATE: 2001-08-07

NUMBER OF SEQ ID NOS: 213

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 68

LENGTH: 693

TYPE: PRT

ORGANISM: Borrelia burgdorferi

US-11-196-475-68

Query Match 7.3%; Score 64.5; DB 7; Length 693;

Best Local Similarity 27.1%; Pred. No. 30;

Matches 36; Conservative 21; Mismatches 53; Indels 23; Gaps 7;

Qy 36 KEAVLRAIDGINQRSSDANLYRLDLDPRPTMGDPDPK-PVSVFTVETVCPRTTQSP 94

Db 324 REKIQEDIDEINK-----EKNL-----PKP---GDVSSPKVDKQLQIKESLEDLQELKE 370

Qy 95 EDCDFKKDGLVKRCMGTVTLNQARSGFDISCDKDKRALLGDFPK--SKEKI-GKEFK 151

Db 371 TSDENQKREIEKQ-----IEIKSDELLKSKOPKALDNLNGLSKRVSSKEKIKGEKE 424

Qy 152 RIVQRIKDFLRNL 164

Db 425 IVKESKASLADL 437

RESULT 9

US-11-052-554A-356

Sequence 356, Application US/11052554A

Publication No. US20050289866A1

GENERAL INFORMATION:

APPLICANT: Sachdeva, et al.

TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE

TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL

FILE REFERENCE: 30853/40359A

CURRENT APPLICATION NUMBER: US/11/052,554A

CURRENT FILING DATE: 2005-02-07

PRIOR APPLICATION NUMBER: US 60/589,227

PRIOR FILING DATE: 2004-07-20

PRIOR APPLICATION NUMBER: IN 173/DEL/2004

PRIOR FILING DATE: 2004-02-06

NUMBER OF SEQ ID NOS: 763

SOFTWARE: PatentIn version 3.3

SEQ ID NO 356

LENGTH: 325

TYPE: PRT

ORGANISM: Streptococcus mutans UAI59

US-11-052-554A-356

Query Match 7.2%; Score 63; DB 7; Length 325;

Best Local Similarity 22.4%; Pred. No. 15;

Matches 28; Conservative 15; Mismatches 44; Indels 38; Gaps 5;

Qy 13 WSLVLLLLGLVMPALIAIAQVLSYKEAVLRAIDGINQRSSDANLYRLDLDPRPTMGDGD 72

Db 165 WALILLIL-----LALTIISYGVVV-----YNQLQTSNKTEL-----S 199

Qy 73 TPKPVSVFTVETVCPRTTQSPEDCDFKKDGLVKRCMGTVTLNQARSGFDISCDKDKRFP 132

Db 200 TSTKSKDKTKDANSTTQSOTSITTFADGG-----NNITLSNTNGKVEVT-----F 246

Qy 133 ALLGCD 137

Db 247 TLTGCD 251

RESULT 10

US-11-192-967-2

Sequence 2, Application US/11192967

Publication No. US20050262587A1

GENERAL INFORMATION:

APPLICANT: Flannagan, Ronald D.

APPLICANT: Mathis, John P.

APPLICANT: Meyer, Terry E.

TITLE OF INVENTION: Novel Bt Toxin Receptors From

TITLE OF INVENTION: Lepidopteran Insects and Methods of Use

FILE REFERENCE: 35718/204664

CURRENT APPLICATION NUMBER: US/11/192,967

CURRENT FILING DATE: 2005-07-29

PRIOR APPLICATION NUMBER: US/09/715,909

PRIOR FILING DATE: 2000-11-17

PRIOR APPLICATION NUMBER: 60/166,285

PRIOR FILING DATE: 1999-11-18

NUMBER OF SEQ ID NOS: 11

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2

LENGTH: 1717

TYPE: PRT

ORGANISM: Ostrinia nubilalis

US-11-192-967-2

Query Match 7.2%; Score 63; DB 7; Length 1717;

Best Local Similarity 19.7%; Pred. No. 1.6e+02;

Matches 28; Conservative 24; Mismatches 52; Indels 38; Gaps 5;

Qy 5 RDGHSLSGRWSLVLL-----LGLVMPALIAIAQVLSYKEAVLRAIDGINQRSSDANLYRL 59

Db 118 RQNEADQWLSLVITQRQDYETATMQSYVFSIQVEGESQAVLVALEIVN----- 165

Qy 60 DLDPRTMGDGDPPKPVSVFTVETVCPRTTQSPEDCDFK---KDLVKRCMGTVTLNQ 116

Db 166 -----IDNPF-----PILQVVSACVPIPEHGEARLTDCVQVSDRDGEISRTFTFRVDS 214

Qy 117 ARGSFDISCDKDKRFPALLGDF 138

Db 215 SRAA-----DESIFTWVGVEY 229

RESULT 11

US-11-193-715-2

Sequence 2, Application US/11193715

Publication No. US20050260675A1

GENERAL INFORMATION:

APPLICANT: Flannagan, Ronald D.

APPLICANT: Mathis, John P.

APPLICANT: Meyer, Terry E.

TITLE OF INVENTION: Novel Bt Toxin Receptors From

TITLE OF INVENTION: Lepidopteran Insects and Methods of Use

FILE REFERENCE: 35718/204664

CURRENT APPLICATION NUMBER: US/11/193,715

; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: US/09/715,909
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/166,285
; PRIOR FILING DATE: 1999-11-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1717
; TYPE: PRT
; ORGANISM: Ostrinia nubilalis
US-11-193-715-2

Query Match 7.2%; Score 63; DB 7; Length 1717;
Best Local Similarity 19.7%; Pred. No. 1.6e+02;
Matches 28; Conservative 24; Mismatches 52; Indels 38; Gaps 5;
QY 5 RDGSLGRWSLVLL-----LGLVMPLAIQAQLVSKAVLRRAIDGINQRSSDANLYRLL 59
DB 118 RQNEADGGWSLVITQRQYETATMQSVFSTQVEGESQAVLVLSIVN----- 165
QY 60 DLDPRPTWDGPDTPKPVSTVKTVCPRITQQSPEDCDFK---KQGLVKRCMGTVTLNQ 116
DB 166 -----IDNP-----PILQVVSACVIPHEGEARLTDCVQVSDRDGEISTREMTFRVDS 214
QY 117 ARGSFDISCDKDKRFPALLGDF 138
DB 215 SRAA-----DESIFYMVGEY 229

RESULT 12
US-11-012-762-8
; Sequence 8, Application US/11012762
; Publication No. US20050244815A1
; GENERAL INFORMATION:
; TITLE OF INVENTION: Compositions and Methods for Viral Resistance Genes
; FILE REFERENCE: GSUI.PCT
; CURRENT APPLICATION NUMBER: US/11/012,762
; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: PCT/US03/19300
; PRIOR FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: US 60/390,046
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 874
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-762-8

Query Match 7.1%; Score 62.5; DB 7; Length 874;
Best Local Similarity 26.3%; Pred. No. 69;
Matches 20; Conservative 11; Mismatches 28; Indels 17; Gaps 2;
QY 94 PEDCDFKDK-----GLVKRCMGTVTLNQARGSFDISCDKDKRFPALLGDF 138
DB 678 PKDFDSERGLSVSGAGFAEQVAGAVLDLMDQEAQMSRQQLKWRKKRFP--VQQS 735
QY 139 FRKSKKIKGKFKRIV 154
DB 736 QQEDKKIKTESGRFI 751

RESULT 13
US-11-033-365-198
; Sequence 198, Application US/11033365
; Publication No. US20050250678A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David

; APPLICANT: Wang, ZhiGuang
; APPLICANT: Clausen, Henrik
; TITLE OF INVENTION: O-Linked Glycosylation of peptides
; FILE REFERENCE: 040853-01-5138
; CURRENT APPLICATION NUMBER: US/11/033,365
; CURRENT FILING DATE: 2005-01-10
; PRIOR APPLICATION NUMBER: 60/535,284
; PRIOR FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: 60/544,411
; PRIOR FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: 60/546,631
; PRIOR FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/555,813
; PRIOR FILING DATE: 2004-03-23
; PRIOR APPLICATION NUMBER: 60/570,891
; PRIOR FILING DATE: 2004-05-12
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 198
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-033-365-198

Query Match 7.1%; Score 62; DB 7; Length 192;
Best Local Similarity 25.7%; Pred. No. 9.6;
Matches 39; Conservative 24; Mismatches 37; Indels 52; Gaps 10;
QY 14 SLVLLGLVMPLAIQAQLVSKAV--LRAI--DGINQRSSDANLYRLL-DLDRPTMD 68
DB 73 NLELRISLLL-----IQSWLPVQFLRSVFANSIVYGASDSNVYDLKDL-----E 120
QY 69 GDDPTPKPVSTVKTVCPRITQQSPEDCDFKQGLVKRCMGTVTLNQARGSFDISCDK 128
DB 121 G-----IQTLGRLEDGSPPT-----TQIFKQTSYKFDNNSHD 154
QY 129 NKRFPALLGDF-----FRKSKKIKGKFKRIVQ 155
DB 155 D---ALLKNYGLLYCFRQMDKDV-ETFLRIVQ 182

RESULT 14
US-11-033-365-200
; Sequence 200, Application US/11033365
; Publication No. US20050250678A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Wang, ZhiGuang
; APPLICANT: Clausen, Henrik
; TITLE OF INVENTION: O-Linked Glycosylation of peptides
; FILE REFERENCE: 040853-01-5138
; CURRENT APPLICATION NUMBER: US/11/033,365
; CURRENT FILING DATE: 2005-01-10
; PRIOR APPLICATION NUMBER: 60/535,284
; PRIOR FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: 60/544,411
; PRIOR FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: 60/546,631
; PRIOR FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/555,813
; PRIOR FILING DATE: 2004-03-23
; PRIOR APPLICATION NUMBER: 60/570,891
; PRIOR FILING DATE: 2004-05-12
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 200
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-033-365-200

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases: older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_NA_Main) and **.rapbn** (Published_Applications_NA_New).
Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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